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Remarks:

A request for correction of the claims (typographical errors claim 15) has been filed pursuant to Rule 88 EPC. A decision on the request will be taken during the proceedings before the Examining Division (Guidelines for Examination in the EPO, A-V, 3.).

(54) ExPEC-specific proteins, genes encoding them and uses thereof

(57) The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of:

- 1-selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
- 2-identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- 3-purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D

isolates,
4- testing the polypeptides for immunogenicity using animals models.

Application for making vaccines compositions.

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Description

[0001] The invention relates to new products specific to pathogenic strains, particularly to extra-intestinal *E. coli* strains.

5 It more particularly relates as products to antigenic polypeptides and antibodies directed against said polypeptides and to their use as vaccines and in immunotherapy, respectively.

[0002] Although *Escherichia coli* is probably the best known bacterial species and is one of the most common isolates in clinical microbiology laboratories, misconceptions abound regarding the various types of *E. coli* and the infections they cause.

10 [0003] *E. coli* strains of biological significance to humans can be broadly considered as constituting 3 major groups:

1. Commensal strains, which are part of the normal flora.

2. Intestinal pathogenic strains, which are not part of the normal flora. This group contains various pathotypes (EPEC, EHEC, ETEC, EIEC) not including *Shigella*.

15 3. Extra-intestinal strains (ExPEC) which are responsible for infections outside the gastro-intestinal (GI) tract, but can also be part of the normal flora. All hosts are susceptible to these infections, immunocompromised and normal.

[0004] ExPEC strains are responsible for the majority of the urinary tract infections (UTI) particularly cystitis, pyelonephritis, and cathether associated infections.

20 [0005] They are also responsible for abdominal infections, nosocomial pneumoniae, neonatal meningitidis, soft tissue infections, and bone infections. Each one of these localizations can lead to bacteremia with a risk of sepsis in case of organ failure. ExPEC strains are indeed the most common Gram negative bacilli isolated from blood cultures.

25 750 000 cases of bacterial sepsis occur each year in the US, and are responsible for 225 000 deaths. In a recent study on 1690 cases of sepsis, it was shown that the main bacteria species identified is ExPEC (16% of the cases) and then *S.aureus* (14% of the cases).

30 [0006] These numbers demonstrate the importance of ExPEC strains in both hospital and community acquired infections.

35 [0007] ExPEC strains correspond to a homogenous subset of *E. coli* strains. Analysis of phylogenetic relationships among *E. coli* strains by MLEE has revealed that *E. coli* belong to 4 main phylogenetic groups designated A, B1, B2 and D.

The pathogenesis of ExPEC strains is that of extra-cellular microorganisms, i.e., they are well adapted to growth in the extra-cellular fluids and efficiently resist phagocytosis by polymorphonuclear. Initial studies have shown that virulence factors known to be important for the extra-cellular growth are mainly found in B2/D *E. coli*, thus suggesting that B2/D subgroups contain most of the ExPEC strains. This was reinforced by experiments performed on animals showing that B2/D strains are more virulent than A and B1 strains. Subsequent epidemiological studies have indeed confirmed these hypotheses. B2/D isolates are those predominantly responsible for neonatal meningitidis (87%) and community or nosocomial acquired urosepsis, (93 % and 85%, respectively). Surprisingly, similar results have been reported for cystitis (70% are due to the sole B2 *E. coli*), thus demonstrating that the pathogenesis of ExPEC strains is that of extra-cellular organisms.

40 These recent findings demonstrate that the B2/D subgroup of strains is the *E. coli* core genome the best adapted to growth in extra-cellular fluids.

45 [0008] In addition to this core genome, ExPEC strains have various pathogenicity islands which encode virulence factors associated with the different pathogenesis of extra-intestinal *E. coli* infections (UTI, urosepsis, neonatal meningitidis...). Among the main virulence factors are the capsule, which is well-known to be important for extra-cellular growth, and the iron chelation systems (aerobactin and enterochelin, for example). In addition, depending on the pathogenesis, these strains can produce toxins (CNF, hemolysin...), adhesins (pap, sfa...) and other iron chelation system.

50 [0009] The notion that B2/D *E. coli* correspond to a distinct subset of pathogenic *E. coli* strains is reinforced by the fact that B2/D *E. coli* are not broadly isolated from the stools of humans. They were recovered from only 11% of individuals, whereas A and B1 subgroups are present in the stools of 74% of the individuals of a human population.

55 [0010] As mentioned above the pathogenesis of ExPEC strains relies on their ability to multiply in the extra-cellular fluids and to resist bactericidal activity of the complement and phagocytosis by polymorphonuclear. Therefore, as for other extra-cellular pathogens (*Haemophilus influenzae*, *Streptococcus pneumoniae* and *meningitidis*) a protective antigen against ExPEC has to induce antibodies that promote opsonisation and/or the bactericidal activity of serum.

[0011] Considering the above statements, an efficient antigen has to be largely represented among the population of B2/D *E. coli*. Similarly to other extra-cellular pathogens, the capsular polysaccharide would be an ideal antigen, however most pathogenic B2 strains express the K1 polysaccharide. The latter has a structure identical to that of group B meningococcus, which is non-immunogenic and shares common antigens with the brain. Another possible target may be the lipopolysaccharide (LPS). However there are a large number of different LPS serotypes that are shared

by various subgroups.

[0012] The inventors have found that components coded by the B2/D genome, but absent from A and B1 *E. coli* strains, are useful as antigens and can specifically prevent the pathologies due to ExPEC strains. It has also been found that homologous antigenic components coded by other pathogenic strains are useful to prevent the pathologies caused by such strains. Accordingly, any reference to products specific to ExPEC strains, and their uses will encompasses such strains.

[0013] It is then an object of the invention to provide isolated antigenic polypeptides and polynucleotides belonging to the core B2/D genome and not present in commensal *E. coli*.

[0014] Another object of the invention is to provide antibodies raised against such antigenic polypeptides.

[0015] It is still another object of the invention to provide vectors and host cells containing said polynucleotides.

[0016] Another object of the invention is to provide vaccine compositions specific to extra intestinal infections caused by ExPEC and pathologies caused by other pathogenic strains expressing antigenic polypeptides homologous to the ExPEC antigenic polypeptides.

[0017] The invention also relates to means for detecting and treating a development of *E. coli* in a human or animal compartment which is extra-intestinal (systemic and non-diarrhoeal infections, such as septicaemia, pyelonephritis, or meningitis in the newborn).

[0018] The isolated antigenic polypeptides of the invention are specific to B2/D *E. coli* strains and not present in A and B1 isolates of *E. coli*. They are encoded by genes belonging to the core B2/D genome and are not present in commensal *E. coli*.

[0019] They have a sequence selected in the group comprising the sequences SEQ ID N°11 to N°66 or homologous sequences with a minimum of 40% of identity with the whole sequences SEQ ID N°11 to N°66, respectively.

[0020] Said polypeptides are obtainable by a process comprising the steps of

- 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
- 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in the B2/D isolates,
- 4- testing the polypeptides for immunogenicity using animals models.

[0021] By the term "conserved", it is meant, according to the invention, that the genes coding for the polypeptides are present with a frequency of at least 50% in B2/D isolates, preferably greater than 60%, more preferably greater than 80% and even more preferably greater than 85%, and in less than 40% in A/B isolates, preferably in less than 20%, more preferably in less than 15%.

[0022] The animal models used in step 4 are infected adult animals, eventually immunodepressed and as models for neonatal infections infant animals.

[0023] The adult animals particularly mice, are infected intraperitoneally, the endpoint being the animal death and/or bacteraemia measurement.

[0024] The animals can be immunodepressed by injection, for example, of cyclophosphamide which induces a neutropenia. Such a model will validate the use of the antigen for prevention of *E. coli* sepsis in immunodepressed patients.

[0025] The second animal model is for example 2 to 3 day old infant mice.

[0026] The variants or fractionnal sequences conserving the B2/D properties and which are antigenic as defined in step 4 of the above process are also part of the invention. The term "variant" is herein intended to mean any sequence having insertions and/or deletions and/or substitutions with respect to the parent sequence. The term "fractional" is herein intended to mean any fragment of the parent sequence.

[0027] Said polynucleotides have preferably sequences corresponding to SEQ ID N°67 to SEQ ID N°132.

[0028] The present application is also aimed towards any vector comprising at least one of said polynucleotides and also any cell transformed by genetic engineering, characterized in that it comprises, by transfection, at least one of said polynucleotides and/or at least one vector according to the invention, and/or in that said transformation induces the production by this cell of at least one polypeptide corresponding to a polynucleotide such as above-defined.

[0029] The invention also relates to a process for isolating and identifying antigenic polypeptides, therefore useful as vaccine for *E. coli*.

[0030] Such a process comprises the steps of

- 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,

- 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates,
- 4- testing the polypeptides for immunogenicity using animals models.

- 5 [0031] The selected antigenic polypeptides, alone or in combination, are capable of inducing an antibody response for prevention of infections due to ExPEC strains regardless of the pathogenesis and the infection site (UTI, pyelonephritis, sepsis, bacteremia, neonatal meningitis).
- [0032] Such polypeptides particularly have sequences SEQ ID N°1 to SEQ ID N°66 or correspond to homologous sequences.
- 10 [0033] The invention thus relates to vaccine compositions specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide as above defined with a carrier, particularly at least one polypeptide of SEQ ID N°1 to SEQ ID N°66 and the homologous sequences.
- [0034] Such vaccine compositions are particularly useful for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.
- 15 [0035] The vaccine compositions of the invention are indicated for
 - immunodepressed patients, ideally before the start of the immunosuppressive therapy : patients suffering from cancer, leukaemia, transplant patients, patients receiving long-term steroids therapy. The *E. coli* vaccine could then be administered in association with a *Staphylococcus aureus* vaccine.
 - patients before surgery where there is a high risk of *E. coli* infections (abdominal surgery)
 - patients with recurrent UTI, especially after one episode of pyelonephritis. The prevention of neonatal infections will require vaccination of the mother, implying vaccination long before pregnancy to avoid potential problem. Ideally such a vaccine should be associated with a Group B *Streptococcus* polysaccharide vaccine in order to also prevent late onset neonatal infections. It should be pointed out that the induction of a level of antibodies against B2/D *E. coli* in pregnant women would also prevent UTI, which are always a risk in the context of a pregnancy.
- 20 [0036] The formulation and the dose of said vaccine compositions can be developed and adjusted by those skilled in the art as a function of the indication targeted, of the method of administration desired, and of the patient under consideration (age, weight).
- 25 [0037] These compositions comprise one or more physiologically inert vehicles, and in particular any excipient suitable for the formulation and/or for the method of administration desired.
- [0038] The antibodies raised against the above-identified polypeptides are also part of the invention.
- 30 [0039] They are capable of binding to said polypeptides in physiological-type conditions (*in vivo* or mimicking *in vivo*) when administered to a human or animal organism, and ELISA-type conditions when said binding product is intended to be used in assays and methods *in vitro*. Such antibodies advantageously inhibit the extra-intestinal growth of ExPEC strains in human or animal.
- 35 [0040] The methods for manufacturing such antibodies using the polypeptides according to the invention are available to those skilled in the art. They are conventional methods which comprise, in particular, the immunization of animals such as rabbits and the harvesting of the serum produced, followed optionally by the purification of the serum obtained. A technique suitable for the production of monoclonal antibodies is that of Köhler and Milstein (Nature 1975, 256:495-497).
- 40 [0041] Said antibodies do not recognize the cells of the human or animal to which it is intended.
- [0042] The antibodies or fragments thereof are advantageously humanized when intended for a human administration.
- 45 [0043] The present invention is also aimed towards the use, in an effective amount, of at least one of said polypeptides, antibodies or polynucleotides for the diagnosis of the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection.
- [0044] The detection of the presence or absence of such compounds can in particular be carried out by nucleotide hybridization, by PCR amplification or by detection of their polypeptide products. Detection of the presence of such compounds makes it possible to conclude that a B2/D *E. coli* strain is present.
- 50 [0045] The present application is also aimed towards any use of a polypeptide such as above defined for the manufacture of a composition, in particular of a pharmaceutical composition, intended to alleviate and/or to prevent and/or to treat an undesirable growth of *E. coli*, such as an *E. coli* infection, (for example systemic and non-diarrhoeal infections), the presence of extra-intestinal *E. coli* or a sanitary contamination.
- 55 [0046] The present invention is illustrated by the examples which follow and which are given in a non limiting capacity.

Example 1: Assay for the immunogenicity of a selected polypeptide from sequences 1-66.

. cloning expression and purification of the selected polypeptide.

5 [0047] The nucleic acid having SEQ ID N°95 encoding the polypeptide corresponding to SEQ ID N°28 was cloned without the signal sequence (coding the 16 first amino acid) in a prokaryotic expression vector according to classical methods for cloning. The recombinant plasmid was used to transform the *E. coli* strain BL21. Transformed cells containing the recombinant plasmid were selected in LB medium with 100µg/ml ampicillin. Individual clones are picked and grown in presence of IPTG 1mM to induce recombinant protein expression. Total protein content of the culture 10 cells was extracted by cell lysis. Recombinant protein was purified by affinity columns.

. Test for immunogenicity in an animal model

15 [0048] Polypeptide preparation from SEQ ID N°28 was injected to Swiss mice to induce an antibody response as follows :

At d0 a first immunisation was done by injecting 20µg of the protein at in 100µg solution of PBS and complet Freund adjuvant (1:1). Control animals were injected with 100µl solution of PBS and complet Freund adjuvant (1:1).

Boosting injection at d21 with 10µg of protein in 100µl PBS and complet Freund adjuvant (1:1).

20 [0049] - Sera from vaccinated animals was prepared from blood drawn by puncture in the tail of the mice.
[0050] Detection of specific antibodies in animal sera, at d20 before the boosting injection, was performed by western blot according to standart protocol. Purified polypeptide was subjected to electrophoresis (10µg per lane) and transfert to nitrocellulose membrane.

25 [0051] The membranes were then saturated by incubation 35 min with PBS/Tween20 0.1%/powder milk 5%.

[0052] Diluted sera was incubated with the membrane for 45 min. Membranes were washed three time 5 min with PBS/tween. Bound antibodies were then recognized by an anti-mouse IgG coupled to horseradish peroxidase enzyme. After washing 3 times with PBS/Tween and 3 time with PBS, enzymatic activity was revealed by addition of chromogenic substrate DAB and hydrogen peroxide.

30 [0053] Results : Sera from vaccinated animal, diluted at 1/100 revealed a unique band corresponding to the injected polypeptide. No antibody to the polypeptide could be detected in sera from control animals.

[0054] At d42, 300 µl of cyclophosphamide and 200µl at d45 were injected IP in the mice to induce neutropenia in order to increase the susceptibility to the challenge infection.

35 At d46 vaccinated and control mice were challenged by intraperitoneal injection of the wt B2/D strain C5 of *E. coli* at a dose equal to 10 time the LD50 (letal dose).

[0055] - Immunogenicity of the selected polypeptide and protection conferred by vaccination with the selected polypeptide was assessed by the survival of vaccinated animals three days post challenge.

Example 2 : Vaccines compositions intending for prevention of any form of infection by ExPEC.

40 [0056] The polypeptide coded by a sequence comprising SEQ ID N°28 is conjugated with a toxin and added to a physiologically inert vehicle.

[0057] This conjugated peptide is optionnally added to a childhood vaccine.

[0058] The composition is sterilized and can be injected parenterally, subcutaneously or intramuscularly.

45 [0059] Said composition can also be sprayed onto mucosa with the aid of a spray.

SEQUENCE LISTING

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40 Leu Ile Leu Asp Gly Ser Val Asn Thr Lys Asn Asp Val Glu Val Ser
545 550 555 560

45 Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe
565 570 575

Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp
580 585 590

50 Trp Val Thr Val Leu Lys Glu Thr Glu Ser Ser Tyr Asn Lys Lys Phe
595 600 605

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Asn Ser Asp Tyr Lys Ser Asn Asn Gln Gln Thr Ser Phe Asp Gln Pro
 610 615 620

5 Asp Trp Lys Thr Gly Val Phe Lys Phe Asp Thr Leu His Leu Asn Asn
 625 630 635 640

10 Ala Asp Phe Ser Ile Ser Arg Asn Ala Asn Val Glu Gly Asn Ile Ser
 645 650 655

Ala Asn Lys Ser Ala Ile Thr Ile Gly Asp Lys Asn Val Tyr Ile Asp
 660 665 670

15 Asn Leu Ala Gly Lys Asn Ile Thr Asn Asn Gly Phe Asp Phe Lys Gln
 675 680 685

20 Thr Ile Ser Thr Asn Leu Ser Ile Gly Glu Thr Lys Phe Thr Gly Gly
 690 695 700

25 Ile Thr Ala His Asn Ser Gln Ile Ala Ile Gly Asp Gln Ala Val Val
 705 710 715 720

Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp
 725 730 735

30 Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly
 740 745 750

35 Ile Asp Ile Ser Gly Glu Leu Thr Met Met Gly Ile Pro Glu Gln Asn
 755 760 765

40 Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg
 770 775 780

Leu Ser Gly Gly Asn Ala Asn Phe Ile Ala Arg Asn Met Ala Ser Val
 785 790 795 800

45 Thr Gly Asn Ile Tyr Ala Asp Asp Ala Ala Thr Ile Thr Leu Gly Gln
 805 810 815

50 Pro Glu Thr Glu Thr Pro Thr Ile Ser Ser Ala Tyr Gln Ala Trp Ala
 820 825 830

Glu Thr Leu Leu Tyr Gly Phe Asp Thr Ala Tyr Arg Gly Ala Ile Thr

55

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5	835	840	845
	Ala Pro Lys Ala Thr Val Ser Met Asn Asn Ala Ile Trp His Leu Asn 850	855	860
10	Ser Gln Ser Ser Ile Asn Arg Leu Glu Thr Lys Asp Ser Met Val Arg 865	870	875
	Phe Thr Gly Asp Asn Gly Lys Phe Thr Thr Leu Thr Val Asn Asn Leu 885	890	895
15	Thr Ile Asp Asp Ser Ala Phe Val Leu Arg Ala Asn Leu Ala Gln Ala 900	905	910
20	Asp Gln Leu Val Val Asn Lys Ser Leu Ser Gly Lys Asn Asn Leu Leu 915	920	925
	Leu Val Asp Phe Ile Glu Lys Asn Gly Asn Ser Asn Gly Leu Asn Ile 930	935	940
25	Asp Leu Val Ser Ala Pro Lys Gly Thr Ala Val Asp Val Phe Lys Ala 945	950	955
30	Thr Thr Arg Ser Ile Gly Phe Ser Asp Val Thr Pro Val Ile Glu Gln 965	970	975
35	Lys Asn Asp Thr Asp Lys Ala Thr Trp Thr Leu Ile Gly Tyr Lys Ser 980	985	990
	Val Ala Asn Ala Asp Ala Ala Lys Lys Ala Thr Leu Leu Met Ser Gly 995	1000	1005
40	Gly Tyr Lys Ala Phe Leu Ala Glu Val Asn Asn Leu Asn Lys Arg 1010	1015	1020
45	Met Gly Asp Leu Arg Asp Ile Asn Gly Glu Ser Gly Ala Trp Ala 1025	1030	1035
50	Arg Ile Ile Ser Gly Thr Gly Ser Ala Gly Gly Phe Ser Asp 1040	1045	1050
	Asn Tyr Thr His Val Gln Val Gly Ala Asp Asn Lys His Glu Leu 1055	1060	1065

5

Asp Gly Leu Asp Leu Phe Thr Gly Val Thr Met Thr Tyr Thr Asp
 1070 1075 1080

10

Ser His Ala Gly Ser Asp Ala Phe Ser Gly Glu Thr Lys Ser Val
 1085 1090 1095

15

Gly Ala Gly Leu Tyr Ala Ser Ala Met Phe Glu Ser Gly Ala Tyr
 1100 1105 1110

15

Ile Asp Leu Ile Gly Lys Tyr Val His His Asp Asn Glu Tyr Thr
 1115 1120 1125

20

Ala Thr Phe Ala Gly Leu Gly Thr Arg Asp Tyr Ser Ser His Ser
 1130 1135 1140

20

Trp Tyr Ala Gly Ala Glu Val Gly Tyr Arg Tyr His Val Thr Asp
 1145 1150 1155

25

Ser Ala Trp Ile Glu Pro Gln Ala Glu Leu Val Tyr Gly Ala Val
 1160 1165 1170

30

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr
 1175 1180 1185

35

Met Lys Asp Lys Asp Phe Asn Pro Leu Ile Gly Arg Thr Gly Val
 1190 1195 1200

35

Asp Val Gly Lys Ser Phe Ser Gly Lys Asp Trp Lys Val Thr Ala
 1205 1210 1215

40

Arg Ala Gly Leu Gly Tyr Gln Phe Asp Leu Phe Ala Asn Gly Glu
 1220 1225 1230

45

Thr Val Leu Arg Asp Ala Ser Gly Glu Lys Arg Ile Lys Gly Glu
 1235 1240 1245

50

Lys Asp Gly Arg Met Leu Met Asn Val Gly Leu Asn Ala Glu Ile
 1250 1255 1260

Arg Asp Asn Leu Arg Phe Gly Leu Glu Phe Glu Lys Ser Ala Phe
 1265 1270 1275

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Gly Lys Tyr Asn Val Asp Asn Ala Ile Asn Ala Asn Phe Arg Tyr
 1280 1285 1290

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Ser Phe
 1295

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<210> 6
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Met Ile Asn Ile Pro Ser Pro Thr Ala Val Val Met Ala Leu Val Ala
 15 10 15
 1 5

Ile Ser Thr Leu Pro Ser Pro Arg Val Lys Leu Met Pro Tyr Pro
 20 25 30

Pro Arg Ala His Asn Thr Thr Gly Leu Leu Pro Val Arg Glu Ile Cys
 35 40 45

25

Phe Pro His His Gly Asp Asp Gly Arg Asn Ser Ile Glu Pro Ser Ile
 50 55 60

Ser Arg Ala Ala His Thr Asp Arg Leu Arg Phe Val Cys Met Thr Arg
 65 70 75 80

Thr Gly Ser Thr Thr Ser Arg Pro Phe Cys Pro Ile Pro Arg Ser Pro
 85 90 95

35

Ala Leu Asn Ala Ser Gly Gln Gln Asp Ser Gly Phe Trp Gly Val Ser
 100 105 110

40

Ser Ile Pro Gly Asp Ile Leu Met Phe Gln Leu His Val Leu Ile Val
 115 120 125

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Phe Ile Cys Lys Ile Asn Leu Ser Asp Asn Asn Ile Ser Tyr
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Met Tyr Ala Arg Glu Tyr Arg Ser Thr Arg Pro His Lys Ala Ile Phe
1 5 10 15

5 Phe His Leu Ser Cys Leu Thr Leu Ile Cys Ser Ala Gln Val Tyr Ala
20 25 30

10 Lys Pro Asp Met Arg Pro Leu Gly Pro Asn Ile Ala Asp Lys Gly Ser
35 40 45

15 Val Phe Tyr His Phe Ser Ala Thr Ser Phe Asp Ser Val Asp Gly Thr
50 55 60

20 Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
65 70 75 80

25 Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
85 90 95

30 Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro
100 105 110

35 Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn
115 120 125

40 Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
130 135 140

45 Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
145 150 155 160

50 Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
165 170 175

55 Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
180 185 190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
195 200 205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
210 215 220

Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Thr Lys His Leu Ala

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225 230 235 240

5 Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala
245 250 255

10 Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp
260 265 270

Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly
275 280 285

15 Pro Met Phe Asn Ala Ser Phe Arg Gln Ala Leu Leu Asp Ile Ser Gly
290 295 300

20 Glu Asn Ala Asn Tyr Thr Ala Gly Cys His Glu Leu Ser His
305 310 315

25 <210> 8
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30 Met Arg Ile Asn Lys Ile Leu Trp Ser Leu Thr Val Leu Leu Val Gly
1 5 10 15

Leu Asn Ser Gln Val Ser Val Ala Lys Tyr Ser Asp Asp Asp Asn Asp
20 25 30

35 Glu Thr Leu Val Val Glu Ala Thr Ala Glu Gln Val Leu Lys Gln Gln
35 40 45

40 Pro Gly Val Ser Val Ile Thr Ser Glu Asp Ile Lys Lys Thr Pro Pro
50 55 60

45 Val Asn Asp Leu Ser Asp Ile Ile Arg Lys Met Pro Gly Val Asn Leu
65 70 75 80

Thr Gly Asn Ser Ala Ser Gly Thr Arg Gly Asn Asn Arg Gln Ile Asp
85 90 95

50 Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Ile Asp Gly Val
100 105 110

55

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Pro Val Thr Ser Arg Asn Ser Val Arg Tyr Ser Trp Arg Gly Glu Arg
 115 120 125

5 Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg
 130 135 140

10 Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala
 145 150 155 160

Ala Gly Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asn Asp Trp
 165 170 175

15 His Gly Ser Leu Ser Leu Tyr Thr Asn Gln Pro Glu Ser Ser Glu Glu
 180 185 190

20 Gly Ala Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Ala Gly
 195 200 205

25 Asp Ala Leu Thr Thr Arg Leu Tyr Gly Asn Leu Asn Lys Thr Asp Ala
 210 215 220

Asp Ser Trp Asp Ile Asn Ser Pro Val Gly Thr Lys Asn Ala Ala Gly
 225 230 235 240

30 His Glu Gly Val Arg Asn Lys Asp Ile Asn Gly Val Val Ser Trp Lys
 245 250 255

35 Leu Asn Pro Gln Gln Ile Leu Asp Phe Glu Val Gly Tyr Ser Arg Gln
 260 265 270

40 Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Ser Ser Ser Ala Val
 275 280 285

Thr Glu Ser Leu Ala Lys Ser Gly Lys Glu Thr Asn Arg Leu Tyr Arg
 290 295 300

45 Gln Asn Tyr Gly Ile Thr His Asn Gly Ile Trp Asp Trp Gly Gln Ser
 305 310 315 320

50 Arg Phe Gly Val Tyr Tyr Glu Lys Thr Asn Asn Thr Arg Met Asn Glu
 325 330 335

Gly Leu Ser Gly Gly Glu Gly Arg Ile Leu Ala Gly Glu Lys Phe

55

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	340	345	350
5	Thr Thr Asn Arg Leu Ser Ser Trp Arg Thr Ser Gly Glu Leu Asn Ile 355	360	365
10	Pro Leu Asn Val Met Val Asp Gln Thr Leu Thr Val Gly Ala Glu Trp 370	375	380
15	Asn Arg Asp Lys Leu Asp Asp Pro Ser Ser Thr Ser Leu Thr Val Asn 385	390	395
20	Asp Arg Asp Ile Ser Gly Ile Ser Gly Ser Ala Ala Asp Arg Ser Ser 405	410	415
25	Lys Asn His Ser Gln Ile Ser Ala Leu Tyr Ile Glu Asp Asn Ile Glu 420	425	430
30	Pro Val Pro Gly Thr Asn Ile Ile Pro Gly Leu Arg Phe Asp Tyr Leu 435	440	445
35	Ser Asp Ser Gly Gly Asn Phe Ser Pro Ser Leu Asn Leu Ser Gln Glu 450	455	460
40	Leu Gly Asp Tyr Phe Lys Val Lys Ala Gly Val Ala Arg Thr Phe Lys 465	470	475
45	Ala Pro Asn Leu Tyr Gln Ser Ser Glu Gly Tyr Leu Leu Tyr Ser Lys 485	490	495
50	Gly Asn Gly Cys Pro Lys Asp Ile Thr Ser Gly Gly Cys Tyr Leu Ile 500	505	510
55	Gly Asn Lys Asp Leu Asp Pro Glu Ile Ser Val Asn Lys Glu Ile Gly 515	520	525
	Leu Glu Phe Thr Trp Glu Asp Tyr His Ala Ser Val Thr Tyr Phe Arg 530	535	540
	Asn Asp Tyr Gln Asn Lys Ile Val Ala Gly Asp Asn Val Ile Gly Gln 545	550	555
	Thr Ala Ser Gly Ala Tyr Ile Leu Lys Trp Gln Asn Gly Gly Lys Ala 565	570	575

Leu Val Asp Gly Ile Glu Ala Ser Met Ser Phe Pro Leu Val Lys Glu
 580 585 590

5

Arg Leu Asn Trp Asn Thr Asn Ala Thr Trp Met Ile Thr Ser Glu Gln
 595 600 605

10

Lys Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Lys Tyr Thr Ile Asn
 610 615 620

15

Asn Ser Leu Asn Trp Thr Ile Thr Gln Ala Phe Ser Ala Ser Phe Asn
 625 630 635 640

Trp Thr Leu Tyr Gly Arg Gln Lys Pro Arg Thr His Ala Glu Thr Arg
 645 650 655

20

Ser Glu Asp Thr Gly Gly Leu Ser Gly Lys Glu Leu Gly Ala Tyr Ser
 660 665 670

25

Leu Val Gly Thr Asn Phe Asn Tyr Asp Ile Asn Lys Asn Leu Arg Leu
 675 680 685

30

Asn Val Gly Val Ser Asn Ile Leu Asn Lys Gln Ile Phe Arg Ser Ser
 690 695 700

Glu Gly Ala Asn Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Gly
 705 710 715 720

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Val Thr Ala Ser Phe
 725

40

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 <213> Escherichia coli
 <400> 9

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Met Gly Asn Gln Trp Gln Gln Lys Tyr Leu Leu Glu Tyr Asn Glu Leu
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50

Val Ser Asn Phe Pro Ser Pro Glu Arg Val Val Ser Asp Tyr Ile Lys
 20 25 30

Asn Cys Phe Lys Thr Asp Leu Pro Trp Phe Ser Arg Ile Asp Pro Asp

55

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	35	40	45
5	Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser 50 55 60		
10	Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr 65 70 75 80		
15	Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe 85 90 95		
20	Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp 100 105 110		
25	Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu 115 120 125		
30	His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu 130 135 140		
35	Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys 145 150 155 160		
40	Asn Tyr Tyr Ile Ser Ser Ala Leu Tyr Leu Tyr Lys Asn Gly Glu Leu 165 170 175		
45	Asp Glu Arg Glu Tyr Asn Phe Ser Met Asn Ala Leu Asn Arg Ser Asp 180 185 190		
50	Asn Ile Ser Leu Leu Phe Phe Asp Ile Tyr Gly Tyr Tyr Ala Ser Asp 195 200 205		
55	Ile Phe Val Ala Lys Asn Asn Asp Lys Val Met Leu Phe Ile Pro Gly 210 215 220		
	Ala Lys Lys Pro Phe Leu Phe Lys Lys Asn Ile Ala Asp Leu Arg Leu 225 230 235 240		
	Thr Leu Lys Glu Leu Ile Lys Asp Ser Asp Asn Lys Gln Leu Leu Ser 245 250 255		
	Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Val Ser Tyr Ala Gly 260 265 270		

5
Val Asn Ser Val Leu His Ala Ile Glu Asn Asp Gly Asn Phe Asn Glu
275 280 285

10
Ser Tyr Phe Leu Tyr Ser Asn Lys Thr Leu Ser Asn Lys Asp Val Phe
290 295 300

15
Asp Ala Ile Ala Ile Ser Val Lys Lys Arg Ser Phe Ser Asp Gly Asp
305 310 315 320

20
Ile Val Ile Lys Ser Asn Ser Glu Ala Gln Arg Asp Tyr Ala Leu Thr
325 330 335

25
Ile Leu Gln Thr Ile Leu Ser Met Thr Pro Ile Phe Asp Ile Val Val
340 345 350

30
Pro Glu Val Ser Val Pro Leu Gly Leu Gly Ile Ile Thr Ser Ser Met
355 360 365

35
Gly Ile Ser Phe Asp Gln Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg
370 375 380

40
Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Ala Val Leu Leu Gly Leu
385 390 395 400

45
Ser Phe Ala Ile Pro Leu Leu Ile Ser Lys Ala Gly Ile Asn Gln Glu
405 410 415

50
Val Leu Ser Ser Val Ile Asn Asn Glu Gly Arg Thr Leu Asn Glu Thr
420 425 430

55
Asn Ile Asp Ile Phe Leu Lys Glu Tyr Gly Ile Ala Glu Asp Ser Ile
435 440 445

60
Ser Ser Thr Asn Leu Leu Asp Val Lys Leu Lys Ser Ser Gly Gln His
450 455 460

65
Val Asn Ile Val Lys Leu Ser Asp Glu Asp Asn Gln Ile Val Ala Val
465 470 475 480

70
Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr
485 490 495

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Gly Tyr Glu Ile Leu Ser Arg Arg Ile Tyr Arg Thr Glu Tyr Asn Asn
500 505 510

5 Glu Ile Leu Trp Thr Arg Gly Gly Leu Lys Gly Gly Gln Pro Phe
515 520 525

10 Asp Phe Glu Ser Leu Asn Ile Pro Val Phe Phe Lys Asp Glu Pro Tyr
530 535 540

15 Ser Ala Val Thr Gly Ser Pro Leu Ser Phe Ile Asn Asp Asp Ser Ser
545 550 555 560

Leu Leu Tyr Pro Asp Thr Asn Pro Lys Leu Pro Gln Pro Thr Ser Glu
565 570 575

20 Met Asp Ile Val Asn Tyr Val Lys Gly Ser Gly Ser Phe Gly Asp Arg
580 585 590

25 Phe Val Thr Leu Met Arg Gly Ala Thr Glu Glu Ala Trp Asn Ile
595 600 605

30 Ala Ser Tyr His Thr Ala Gly Gly Ser Thr Glu Glu Leu His Glu Ile
610 615 620

Leu Leu Gly Gln Gly Pro Gln Ser Ser Leu Gly Phe Thr Glu Tyr Thr
625 630 635 640

35 Ser Asn Val Asn Ser Ala Asp Ala Ala Ser Arg Arg His Phe Leu Val
645 650 655

40 Val Ile Lys Val His Val Lys Tyr Ile Thr Asn Asn Asn Val Ser Tyr
660 665 670

45 Val Asn His Trp Ala Ile Pro Asp Glu Ala Pro Val Glu Val Leu Ala
675 680 685

Val Val Asp Arg Arg Phe Asn Phe Pro Glu Pro Ser Thr Pro Pro Asp
690 695 700

50 Ile Ser Thr Ile Arg Lys Leu Leu Ser Leu Arg Tyr Phe Lys Glu Ser
705 710 715 720

55

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Ile Glu Ser Thr Ser Lys Ser Asn Phe Gln Lys Leu Ser Arg Gly Asn
 725 730 735

5 Ile Asp Val Leu Lys Gly Arg Gly Ser Ile Ser Ser Thr Arg Gln Arg
 740 745 750

10 Ala Ile Tyr Pro Tyr Phe Glu Ala Ala Asn Ala Asp Glu Gln Gln Pro
 755 760 765

Leu Phe Phe Tyr Ile Lys Lys Asp Arg Phe Asp Asn His Gly Tyr Asp
 770 775 780

15 Gln Tyr Phe Tyr Asp Asn Thr Val Gly Leu Asn Gly Ile Pro Thr Leu
 785 790 795 800

20 Asn Thr Tyr Thr Gly Glu Ile Pro Ser Asp Ser Ser Ser Leu Gly Ser
 805 810 815

25 Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg
 820 825 830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu
 835 840 845

30 Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser
 850 855 860

35 Gly Cys Thr Thr Ile Val Ala Arg Lys Glu Gly Tyr Ile Tyr Lys Val
 865 870 875 880

40 His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly
 885 890 895

Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile
 900 905 910

45 Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu
 915 920 925

50 Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys
 930 935 940

55 Lys Pro Asp Ser Gln Ile Thr Ile Ile Arg Asp Asn Val Ser Val Phe

	945	950	955	960
5	Pro Tyr Phe Leu Asp Asn Ile Pro Glu His Gly Phe Gly Thr Ser Ala 965 970 975			
10	Thr Val Leu Val Arg Val Asp Gly Asn Val Val Val Arg Ser Leu Ser 980 985 990			
15	Glu Ser Tyr Ser Leu Asn Ala Asp Ala Ser Glu Ile Ser Val Leu Lys 995 1000 1005			
20	<210> 10 <211> 454 <212> PRT <213> Escherichia coli <400> 10			
25	Met Val Asp Met Ile Asn Glu Ser Ala Arg Gln Thr Pro Val Ile Ala 1 5 10 15			
30	Gln Thr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala 20 25 30			
35	Ala Ile Ala Ala Gly Arg Leu Gly Ala Arg Thr Met Ile Val Glu Arg 35 40 45			
40	Tyr Gly Ser Leu Gly Gly Val Leu Thr Gln Val Gly Val Glu Ser Phe 50 55 60			
45	Ala Trp Tyr Arg His Pro Gly Thr Glu Asp Cys Glu Gly Ile Cys Arg 65 70 75 80			
50	Glu Tyr Glu Gly Arg Ala Arg Ala Leu Gly Phe Thr Arg Pro Glu Pro 85 90 95			
55	Gln Ser Ile Ser Glu Val Ile Asp Thr Glu Gly Phe Lys Val Val Ala 100 105 110			
	Asp Gln Met Ile Thr Glu Ser Gly Val Glu Pro Leu Tyr His Ser Trp 115 120 125			

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Val Val Asp Val Ile Lys Asp Gly Asp Thr Leu Cys Gly Val Ile Val
 130 135 140

5 Glu Asn Lys Ser Gly Arg Gly Ala Ile Leu Ala Lys Arg Ile Val Asp
 145 150 155 160

10 Cys Thr Gly Asp Ala Asp Ile Ala Ala Arg Ala Gly Ala Pro Trp Thr
 165 170 175

Lys Arg Ser Lys Asp Gln Leu Met Gly Val Thr Val Met Phe Ser Cys
 180 185 190

15 Ala Gly Val Asp Val Ala Arg Phe Asn Arg Phe Val Ala Glu Glu Leu
 195 200 205

20 Lys Pro Thr Tyr Ala Asp Trp Gly Lys Asn Trp Thr Ile Gln Thr Thr
 210 215 220

Gly Lys Glu Asp Pro Met Phe Ser Pro Tyr Met Glu Asp Ile Phe Thr
 225 230 235 240

25 Arg Ala Gln Gln Asp Gly Val Ile Pro Gly Asp Ala Gln Ala Ile Ala
 245 250 255

30 Gly Thr Trp Ser Thr Phe Ser Glu Ser Gly Glu Ala Phe Gln Met Asn
 260 265 270

35 Met Val Tyr Ala Phe Gly Phe Asp Cys Thr Asp Val Phe Asp Leu Thr
 275 280 285

Lys Ala Glu Ile Ala Gly Arg Gln Gln Ala Leu Trp Ala Ile Asp Ala
 290 295 300

40 Leu Arg His Tyr Val Pro Gly Phe Glu Asn Val Arg Leu Arg Asn Phe
 305 310 315 320

45 Gly Ala Thr Leu Gly Thr Arg Glu Ser Arg Leu Ile Glu Gly Glu Ile
 325 330 335

50 Arg Ile Ala Asp Asp Tyr Val Leu Asn Gln Gly Arg Cys Ser Asp Ser
 340 345 350

Val Gly Ile Phe Pro Glu Phe Ile Asp Gly Ser Gly Tyr Leu Ile Leu

55

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355

360

365

5 Pro Thr Thr Gly Arg Phe Phe Gln Ile Pro Tyr Gly Cys Leu Val Pro
 370 375 380

10 Gln Lys Val Glu Asn Leu Leu Val Ala Gly Arg Cys Ile Ser Ala Gly
 385 390 395 400

15 Val Val Ala His Thr Ser Met Arg Asn Met Met Cys Cys Ala Val Thr
 405 410 415

20 Gly Glu Ala Ala Gly Thr Ala Ala Val Val Ser Leu Gln Gln Asn Cys
 420 425 430

25 Thr Val Arg Gln Val Ala Ile Pro Asp Leu Gln Asn Thr Leu Gln Gln
 435 440 445

30 Gln Sly Val Arg Leu Ala
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35 <210> 11
 <211> 253
 <212> PRT
 <213> Escherichia coli
 <400> 11

40 Met Ser Ala Lys Arg Arg Leu Leu Ile Ala Cys Thr Leu Ile Thr Ala
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45 Ile Tyr His Phe Pro Ala Tyr Ser Ser Leu Glu Tyr Lys Gly Thr Phe
 20 25 30

50 Gly Ser Ile Asn Ala Gly Tyr Ala Asp Trp Asn Ser Gly Phe Val Asn
 35 40 45

55 Thr His Arg Gly Glu Val Trp Lys Val Thr Ala Asp Phe Gly Val Asn
 50 55 60

60 Phe Lys Glu Ala Glu Phe Tyr Ser Phe Tyr Glu Ser Asn Val Leu Asn
 65 70 75 80

65 His Ala Val Ala Gly Arg Asn His Thr Val Ser Ala Met Thr His Val
 85 90 95

55

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Arg Leu Phe Asp Ser Asp Met Thr Phe Phe Gly Lys Ile Tyr Gly Gln
 100 105 110

5 Trp Asp Asn Ser Trp Gly Asp Asp Leu Asp Met Phe Tyr Gly Phe Gly
 115 120 125

10 Tyr Leu Gly Trp Asn Gly Glu Trp Gly Phe Phe Lys Pro Tyr Ile Gly
 130 135 140

15 Leu His Asn Gln Ser Gly Asp Tyr Val Ser Ala Lys Tyr Gly Gln Thr
 145 150 155 160

Asn Gly Trp Asn Gly Tyr Val Val Gly Trp Thr Ala Val Leu Pro Phe
 165 170 175

20 Thr Leu Phe Asp Glu Lys Phe Val Leu Ser Asn Trp Asn Glu Ile Glu
 180 185 190

25 Leu Asp Arg Asn Asp Ala Tyr Thr Glu Gln Gln Phe Gly Arg Asn Gly
 195 200 205

Leu Asn Gly Gly Leu Thr Ile Ala Trp Lys Phe Tyr Pro Arg Trp Lys
 210 215 220

30 Ala Ser Val Thr Trp Arg Tyr Phe Asp Asn Lys Leu Gly Tyr Asp Gly
 225 230 235 240

35 Phe Gly Asp Gln Met Ile Tyr Met Leu Gly Tyr Asp Phe
 245 250

40 <210> 12
 <211> 492
 <212> PRT
 <213> Escherichia coli
 <400> 12

45 Met Ala Ser Leu Ile Gly Leu Ala Val Cys Thr Gly Asn Ala Phe Ser
 1 5 10 15

50 Pro Ala Leu Ala Ala Glu Ala Lys Gln Pro Asn Leu Val Ile Ile Met
 20 25 30

Ala Asp Asp Leu Gly Tyr Gly Asp Leu Ala Thr Tyr Gly His Gln Ile
 35 40 45

55

Val Lys Thr Pro Asn Ile Asp Arg Leu Ala Gln Glu Gly Val Lys Phe
 50 55 60

5 Thr Asp Tyr Tyr Ala Pro Ala Pro Leu Ser Ser Pro Ser Arg Ala Gly
 65 70 75 80

10 Leu Leu Thr Gly Arg Met Pro Phe Arg Thr Gly Ile Arg Ser Trp Ile
 85 90 95

15 Pro Ser Gly Lys Asp Val Ala Leu Gly Arg Asn Glu Leu Thr Ile Ala
 100 105 110

Asn Leu Leu Lys Ala Cln Gly Tyr Asp Thr Ala Met Met Gly Lys Leu
 115 120 125

20 His Leu Asn Ala Gly Gly Asp Arg Thr Asp Gln Pro Gln Ala Gln Asp
 130 135 140

25 Met Gly Phe Asp Tyr Ser Leu Ala Asn Thr Ala Gly Phe Val Thr Asp
 145 150 155 160

30 Ala Thr Leu Asp Asn Ala Lys Glu Arg Pro Arg Tyr Gly Met Val Tyr
 165 170 175

Pro Thr Gly Trp Leu Arg Asn Gly Gln Pro Thr Pro Arg Ala Asp Lys
 180 185 190

35 Met Ser Gly Glu Tyr Val Ser Ser Glu Val Val Asn Trp Leu Asp Asn
 195 200 205

40 Lys Lys Asp Ser Lys Pro Phe Phe Leu Tyr Val Ala Phe Thr Glu Val
 210 215 220

45 His Ser Pro Leu Ala Ser Pro Lys Lys Tyr Leu Asp Met Tyr Ser Gln
 225 230 235 240

Tyr Met Ser Ala Tyr Gln Lys Gln His Pro Asp Leu Phe Tyr Gly Asp
 245 250 255

50 Trp Ala Asp Lys Pro Trp Arg Gly Val Gly Glu Tyr Tyr Ala Asn Ile
 260 265 270

55

Ser Tyr Leu Asp Ala Gln Val Gly Lys Val Leu Asp Lys Ile Lys Ala
 275 280 285

 5 Met Gly Glu Glu Asp Asn Thr Ile Val Ile Phe Thr Ser Asp Asn Gly
 290 295 300

 10 Pro Val Thr Arg Glu Ala Arg Lys Val Tyr Glu Leu Asn Leu Ala Gly
 305 310 315 320

 15 Glu Thr Asp Gly Leu Arg Gly Arg Lys Asp Asn Leu Trp Glu Gly Gly
 325 330 335

 20 Ile Arg Val Pro Ala Ile Ile Lys Tyr Gly Lys His Leu Pro Gln Gly
 340 345 350

 25 Met Val Ser Asp Thr Pro Val Tyr Gly Leu Asp Trp Met Pro Thr Leu
 355 360 365

 Ala Lys Met Met Asn Phe Lys Leu Pro Thr Asp Arg Thr Phe Asp Gly
 370 375 380

 30 Glu Ser Leu Val Pro Val Leu Glu Gln Lys Ala Leu Lys Arg Glu Lys
 385 390 395 400

 35 Pro Leu Ile Phe Gly Ile Asp Met Pro Phe Gln Asp Asp Pro Thr Asp
 405 410 415

 40 Glu Trp Ala Ile Arg Asp Gly Asp Trp Lys Met Ile Ile Asp Arg Asn
 420 425 430

 Asn Lys Pro Lys Tyr Leu Tyr Asn Leu Lys Ser Asp Arg Tyr Glu Thr
 435 440 445

 45 Leu Asn Leu Ile Gly Lys Lys Pro Asp Ile Glu Lys Gln Met Tyr Gly
 450 455 460

 Lys Phe Leu Lys Tyr Lys Thr Asp Ile Asp Asn Asp Ser Leu Met Lys
 465 470 475 480

 50 Ala Arg Gly Asp Lys Pro Glu Ala Val Thr Trp Gly
 485 490

<210> 13

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<211> 345
 <212> PRT
 <213> Escherichia coli
 <400> 13

5 Leu Ile Ser Leu Ser Phe Ile Pro Val Met Ser Ala Leu Pro Gly Pro
 1 5 10 15

10 Ile Ala Lys Gly Phe Arg Asn Glu Arg Gly Phe Val Thr Thr Thr Ile
 20 25 30

15 Cys Ala Met Gly Glu Leu Leu Ala Glu Phe Leu Ser Arg Asn Pro His
 35 40 45

20 Gln Lys Phe Thr Gln Pro Gly Glu Phe Ile Gly Pro Phe Pro Ser Gly
 50 55 60

25 Ala Pro Ala Ile Phe Ala Ala Gln Val Ala Lys Leu Ser His Arg Ala
 65 70 75 80

30 Ile Phe Phe Gly Cys Val Gly Asn Asp Asp Phe Ala Arg Leu Ile
 85 90 95

35 Glu Arg Leu Arg His Glu Gly Val Ile Thr Asp Gly Ile His Val Met
 100 105 110

40 Asn Asn Ala Val Thr Gly Thr Ala Phe Val Ser Tyr Gln Asn Pro Gln
 115 120 125

45 Gln Arg Asp Phe Val Phe Asn Ile Pro Asn Ser Ala Cys Gly Leu Phe
 130 135 140

50 Thr Ala Glu His Ile Asp Lys Asp Leu Leu Lys Gln Cys Asn His Leu
 145 150 155 160

55 His Ile Val Gly Ser Ser Leu Phe Ser Phe Arg Met Ile Asp Val Met
 165 170 175

Arg Lys Ala Ile Thr Thr Ile Lys Ser Ala Gly Gly Thr Val Ser Phe
 180 185 190

55 Asp Pro Asn Ile Arg Lys Glu Met Leu Ser Ile Pro Glu Met Ala Gln
 195 200 205

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Ala Leu Asp Tyr Leu Ile Glu Tyr Thr Asp Ile Phe Ile Pro Ser Glu
210 215 220

5 Ser Glu Leu Pro Phe Phe Ala Arg His Lys Asn Leu Ser Glu Glu Gln
225 230 235 240

10 Ile Val Ser Asp Leu Leu His Gly Gly Val Lys His Val Ala Ile Lys
245 250 255

Arg Ala Gln Arg Gly Ala Ser Tyr Tyr Lys Leu Lys Asn Gly Thr Leu
260 265 270

15 His Ala Gln His Val Ala Gly His Asp Ile Glu Ile Ile Asp Pro Thr
275 280 285

20 Gly Ala Gly Asp Cys Phe Gly Ala Thr Phe Ile Thr Leu Phe Leu Ser
290 295 300

25 Gly Phe Pro Ala His Lys Ala Leu Gln Tyr Ala Asn Ala Ser Gly Ala
305 310 315 320

Leu Ala Val Met Arg Gln Gly Pro Met Glu Gly Ile Ser Ser Leu Ala
325 330 335

30 Asp Ile Glu Asp Phe Leu Gln Gln His
340 345

35 <210> 14
<211> 192
<212> PRT
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<400> 14

40 Met Tyr Met Pro Gly Lys Gln Met Leu Cys Cys Ile Leu Ile Ser Ile
1 5 10 15

45 Ile Ser Glu Gly Asp Met Lys Ile Phe Ile Ser Leu Phe Leu Phe Ile
20 25 30

50 Ile Ser Thr Asn Ser Phe Ala Asp Asp Ile Thr His Ala Gly Val Val
35 40 45

55 Arg Ile Glu Gly Leu Ile Thr Glu Lys Thr Cys Ile Ile Ser Asp Glu
50 55 60

55

Ser Lys Asn Phe Thr Val Asn Met Pro Asp Val Pro Ser Ser Ser Val
 65 70 75 80

5 Arg Ser Ala Gly Asp Val Thr Glu Lys Val Tyr Phe Ser Ile Thr Leu
 85 90 95

10 Thr Arg Cys Gly Ser Asp Val Gly Asn Ala Tyr Ile Lys Phe Thr Gly
 100 105 110

15 Asn Thr Val Ser Glu Asp Ala Ser Leu Tyr Lys Leu Glu Asp Gly Ser
 115 120 125

Val Glu Gly Leu Ala Leu Thr Ile Phe Asp Lys Asn Lys Gly Ser Ile
 130 135 140

20 Ser Asn Asp Val Lys Ser Met Val Phe Ser Leu Thr Ser Ser Val Asp
 145 150 155 160

25 Asn Ile Leu His Phe Phe Ala Ala Tyr Lys Ala Leu Lys Asn Asn Val
 165 170 175

30 Gln Pro Gly Asp Ala Asn Ala Ser Val Ser Phe Ile Val Thr Tyr Asp
 180 185 190

35 <210> 15
 <211> 201
 <212> PRT
 <213> Escherichia coli
 <400> 15

Met Ile Lys Phe Arg Leu Tyr Ile Pro Pro Val Ile Leu Gly Phe Val
 1 5 10 15

40 Ile Val Pro Leu Leu Val Trp Pro Thr Val Ile Ala Leu Ala Val Leu
 20 25 30

45 Ile Phe Thr Leu Thr Phe Leu Ala Glu Ile Ile Phe Ser Phe Pro Leu
 35 40 45

50 Leu Val Val Arg Ile Ser Leu Gln Glu Leu Gln Leu Glu Leu Val
 50 55 60

55 Val Tyr Ala Leu Phe Phe Ser Val Met Gly Gly Ile Gly Trp Gln Phe
 65 70 75 80

5

Ser Arg Arg Thr Pro Pro Glu Leu Lys Asn Arg Leu His Cys Trp Leu
 85 90 95

Val Phe Ser Pro Val Tyr Phe Trp Leu Ile Leu Ser Asn Phe Ile Leu
 100 105 110

10

Tyr Ile Ser Pro Glu Lys Ser Ala Leu Leu Glu Asn Ile Arg Asn Phe
 115 120 125

15

Phe Leu Thr Phe Val Trp Leu Pro Leu Asn Phe Ser Pro Phe Trp Pro
 130 135 140

20

Gln Pro Trp Thr Asp Phe Val Gly Pro Ile Ser Ala Gln Leu Gly Phe
 145 150 155 160

Ala Leu Gly Tyr Tyr Cys Gln Trp Arg Ser Lys Asn Arg Ser His Arg
 165 170 175

25

Lys Lys Trp Gly Asp Trp Val Thr Cys Leu Ser Leu Ala Ile Leu Ala
 180 185 190

30

Leu Gly Pro Leu Phe Asn Tyr Leu Gln
 195 200

35

<210> 16
 <211> 234
 <212> PRT
 <213> Escherichia coli
 <400> 16

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Met Lys Phe Asn Leu Ser Asn Leu Ser Ala Val Leu Leu Ala Ser Gly
 1 5 10 15

45

Met Leu Met Ser Thr Ala Val Thr Ala Ala Pro Gly Asp Ala Thr Gln
 20 25 30

50

Phe Gly Gly Ala Asp Thr Asp Trp Ser Thr Val Asp Tyr Pro Arg Leu
 35 40 45

55

Thr Asp Met Asp Asp Asn Val Asp Ser Met Gly Gly Lys Ile Arg Phe
 50 55 60

Thr Gly Arg Val Val Lys Ala Thr Cys Lys Val Ala Thr Asp Ser Lys

	65	70	75	80
5	Gln Ile Glu Val Val Leu Pro Val Val Pro Ser Asn Leu Phe Thr Gly 85		90	95
10	Ile Asp Val Glu Ala Gln Gly Ala Ser Asn Gln Thr Asp Phe Asn Ile 100		105	110
15	Asn Leu Thr Glu Cys Ser Asn Thr Asp Asp Gln Lys Ile Glu Phe Arg 115		120	125
20	Phe Thr Gly Thr Ala Asp Ser Ala Asn Lys Thr Leu Ala Asn Glu Val 130	135	140	
25	Glu Gly Ser Thr Asp Ala Asp Asn Ser Gly Asn Ala Gly Ala Thr Gly 145	150	155	160
30	Val Gly Ile Arg Ile Tyr Ser Lys Gly Thr Thr Asn Asn Gly Leu Ile 165	170	175	
35	Asn Leu Asn Thr Thr Ala Ala Glu Gly Ser Ala Ser Thr Ala Ala Tyr 180	185	190	
40	Thr Ile Pro Gly Asn Ala Thr Thr His Asp Phe Ser Ala Ala Phe Thr 195	200	205	
45	Ala Gly Tyr Ala Gln Asn Gly Ser Thr Val Ala Pro Gly Val Val Lys 210	215	220	
50	Ser Thr Ala Ser Phe Val Val Leu Tyr Glu 225	230		
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	Met Arg Ile His Thr Tyr Trp Tyr Arg Arg Tyr Phe Ile Leu Leu Ile 1	5	10	15
	Ile Ile Phe Ser Asn Val Leu Ser Ser Ile Ala Asn Ala Glu Asp Met 20	25	30	

Gly Arg Glu Arg Ala Tyr Cys Tyr Pro Gly Ser Pro Ser Asn Asn Thr
 35 40 45

5 Thr Pro Ala Ser Phe Ser Tyr Asn Phe Gly Thr Ile Val Val Ser Asp
 50 55 60

10 Val Asn Lys Asn Ala Pro Gly Thr Val Leu Pro Ser Gln Ile Trp Lys
 65 70 75 80

15 Val Gly Thr Tyr Lys Ala Tyr Cys Asn Ser Leu Asp Asp Tyr Glu Ile
 85 90 95

20 His Gln Gly Ser Asp Val Phe Ile Pro Leu Thr His Glu Ile Ser Val
 115 120 125

25 Ser Thr His Ile Lys Leu Tyr Asn Gln Asn Gly Thr Met Thr Asp Lys
 130 135 140

30 Ile Val Pro Phe Glu Asn Tyr Asn Thr Asn Tyr Pro Gly Asp Arg Ser
 145 150 155 160

35 Lys Pro Ser Asn Trp Ala Ser Gly Thr Glu Gly Tyr Ile Lys Ile Arg
 165 170 175

40 Ile Asp Lys Lys Ile Ile Ser Asp Val Ser Leu Ser Asn Val Leu Leu
 180 185 190

45 Val Ser Leu Tyr Val Ser Gln Ile Pro Thr Glu His Gly Pro Ile Pro
 195 200 205

50 Val Phe Asn Ala Tyr Ile Gly Asn Leu Asn Ile Gln Val Pro Gln Gly
 210 215 220

55 Cys Thr Ile Asn Glu Gly Thr Ser Phe Thr Val Asn Met Pro Asp Val
 225 230 235 240

Trp Ala Ser Glu Leu Ser Arg Ala Gly Ala Gly Ala Lys Pro Ala Gly
 245 250 255

Val Thr Pro Val Ala Thr Thr Ile Pro Ile Asn Cys Thr Asn Lys Asp

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260

265

270

Thr Asp Ala Val Met Thr Leu Val Phe Asp Gly Asn Ile Ser Ala Thr
 275 280 285

5

Arg Asp Thr Asn Gly Lys Gln Ser Ile Ile Gln Ala Gln Asp Asn Pro
290 295 300

10

Asp Val Gly Ile Met Ile Met Asp Ser Gln Gln Asn Ser Val Asp Leu
 305 310 315 320

15

Asn Ala Leu Ala Thr Ser Val Gly Val Pro Phe Arg Leu Val Glu Asn
 325 330 335

<210> 18
<211> 864
<212> PRT
<213> Escherichia coli
<400> 18

30

Gln Met Lys Arg Val Val Pro Leu Leu Leu Val Ile Met Pro Ala Cys
20 25 30

35

Ser Ile Ala Gly Met Arg Phe Asn Pro Ala Phe Leu Ser Gly Asp Thr
35 40 45

40

Pro Gly Ser Tyr Glu Val Glu Val Trp Val Asn Asp Ser Pro Leu Leu
65 70 75 80

13

Cys Leu Ser Leu Ala Asp Leu Leu Ser Leu Gly Ile Asn Lys Asn Ala
 100 105 110

50

Leu Pro Glu Gln Ala Leu Ala Ser Ser Glu Asn Ser Cys Leu Asp Leu
115 120 125

Arg Ile Trp Phe Pro Asp Val His Tyr Met Pro Glu Leu Asp Ala Gln
 130 135 140

5 Arg Leu Lys Leu Thr Phe Pro Gln Ala Ile Ile Lys Arg Asp Ala Arg
 145 150 155 160

10 Gly Tyr Ile Pro Pro Glu Gln Trp Asp Asn Gly Ile Thr Ala Phe Leu
 165 170 175

Leu Asn Tyr Asp Phe Ser Gly Asn Asn Asp Arg Gly Asp Tyr Ser Ser
 180 185 190

15 Asn Asn Tyr Tyr Leu Asn Leu Arg Ala Gly Ile Asn Ile Gly Ala Trp
 195 200 205

20 Arg Phe Arg Asp Tyr Ser Thr Trp Ser Arg Gly Ser Asn Ser Ala Gly
 210 215 220

25 Lys Leu Glu His Ile Ser Ser Thr Leu Gln Arg Val Ile Ile Pro Phe
 225 230 235 240

Arg Ser Glu Leu Thr Leu Gly Asp Thr Trp Ser Ser Ser Asp Val Phe
 245 250 255

30 Asp Ser Val Ser Ile Arg Gly Ile Lys Leu Glu Ser Asp Glu Asn Met
 260 265 270

35 Leu Pro Asp Ser Gln Ser Gly Phe Ala Pro Thr Val Arg Gly Ile Ala
 275 280 285

40 Lys Ser Arg Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Val Ile Tyr
 290 295 300

Gln Thr Tyr Met Pro Pro Gly Pro Phe Glu Ile Ser Asp Leu Asn Pro
 305 310 315 320

45 Thr Ser Ser Ala Gly Asp Leu Glu Val Thr Ile Lys Glu Ser Asp Asn
 325 330 335

50 Ser Glu Thr Val Tyr Thr Val Pro Tyr Ala Ala Val Pro Ile Leu Gln
 340 345 350

Arg Glu Gly His Leu Lys Tyr Ser Thr Thr Val Gly Gln Tyr Arg Ser

55

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355 360 365

5 Asn Ser Tyr Asn Gln Lys Ser Pro Tyr Val Phe Gln Gly Glu Leu Ile
 370 375 380

10 Trp Gly Leu Pro Trp Asp Ile Thr Ala Tyr Gly Gly Ala Gln Phe Ser
 385 390 395 400

15 Glu Asp Tyr Arg Ala Leu Ala Leu Gly Leu Asn Leu Gly Val
 405 410 415

20 Phe Gly Ala Thr Ser Phe Asp Val Thr Gln Ala Asn Ser Ser Leu Val
 420 425 430

25 Asp Gly Ser Lys His Gln Gly Gln Ser Tyr Arg Phe Leu Tyr Ser Lys
 435 440 445

30 Ser Leu Val Gln Thr Gly Thr Ala Phe His Ile Ile Gly Tyr Arg Tyr
 450 455 460

35 Ser Thr Gln Gly Phe Tyr Thr Leu Ser Asp Thr Thr Tyr Gln Gln Met
 465 470 475 480

40 Ser Gly Thr Val Val Asp Pro Lys Thr Leu Asp Asp Lys Asp Tyr Val
 485 490 495

45 Tyr Asn Trp Asn Asp Phe Tyr Asn Leu Arg Tyr Ser Lys Arg Gly Lys
 500 505 510

50 Phe Gln Ala Ser Val Ser Gln Pro Phe Gly Asn Tyr Gly Ser Met Tyr
 515 520 525

55 Leu Ser Ala Ser Gln Gln Thr Tyr Trp Asn Thr Asp Lys Asp Ser
 530 535 540

60 Leu Tyr Gln Val Gly Tyr Asn Thr Ser Ile Lys Gly Ile Tyr Leu Asn
 545 550 555 560

65 Val Ala Trp Asn Tyr Ser Lys Ser Pro Gly Thr Asn Ala Asp Lys Ile
 565 570 575

70 Val Ser Leu Asn Val Ser Leu Pro Ile Ser Asn Trp Leu Ser Ser Thr
 580 585 590

5

Asn Asp Gly Arg Ser Ser Ser Asn Ala Met Thr Ala Thr Tyr Gly Tyr
 595 600 605

10

Ser Gln Asp Asn His Gly Gln Val Asn Gln Tyr Thr Gly Val Ser Gly
 610 615 620

15

Ser Leu Leu Glu Gln His Asn Leu Ser Tyr Asn Ile Gln His Gly Phe
 625 630 635 640

20

Ala Asn Gln Asp Asn Ser Ser Ser Gly Ser Val Gly Val Asn Tyr Arg
 645 650 655

25

Gly Ala Tyr Gly Ser Leu Asn Ser Ala Tyr Ser Tyr Asp Asn Glu Gly
 660 665 670

30

Asn Gln Gln Ile Asn Tyr Gly Ile Ser Gly Ala Leu Val Val His Glu
 675 680 685

35

Asn Gly Leu Thr Leu Ser Gln Pro Leu Gly Glu Thr Asn Val Leu Ile
 690 695 700

40

Lys Ala Pro Gly Ala Asn Asn Val Asp Val Gln Arg Gly Thr Gly Ile
 705 710 715 720

45

Ser Thr Asp Trp Arg Gly Tyr Ala Val Val Pro Tyr Ala Thr Glu Tyr
 725 730 735

50

Arg Arg Asn Asn Ile Ser Leu Asp Pro Met Ser Met Asn Met His Thr
 740 745 750

55

Glu Leu Asp Ile Thr Ser Thr Glu Val Ile Pro Gly Lys Gly Ala Leu
 755 760 765

60

Val Arg Ala Glu Phe Ala Ala His Ile Gly Ile Arg Gly Leu Phe Thr
 770 775 780

65

Val Arg Tyr Arg Asn Lys Ser Val Pro Phe Gly Ala Thr Ala Ser Ala
 785 790 795 800

70

Gln Ile Lys Asn Ser Ser Gln Ile Thr Gly Ile Val Gly Asp Asn Gly
 805 810 815

75

Gln Leu Tyr Leu Ser Gly Leu Pro Leu Glu Gly Val Ile Asn Ile Gln
 820 825 830
 5 Trp Gly Asp Gly Val Gln Lys Cys Gln Ala Asn Tyr Lys Leu Pro
 835 840 845
 10 Glu Thr Glu Leu Asp Asn Pro Val Ser Tyr Ala Thr Leu Glu Cys Arg
 850 855 860
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 <211> 169
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 <213> Escherichia coli
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 20 Met Gly Ala Ile Tyr Val Lys Arg Leu Ile Leu Ser Val Ala Leu Ile
 1 5 10 15
 Ile Pro Ile Ala Ser Asn Ala Ser Asp Ala Leu Asn Gln Pro Ser Ser
 20 25 30
 25 Ser Leu Asn Asp Gly Val Glu Thr Phe Phe Ile Ser Cys Phe Asp Met
 35 40 45
 30 Pro Gln Glu Thr Thr Asp Met Asp Ala Cys Gln Arg Val Gln Leu
 50 55 60
 35 Ala Gln Val Ser Trp Val Lys Asn Lys Tyr Ser Val Ala Ala Leu Asn
 65 70 75 80
 Arg Leu Lys Gln Asp Asn Lys Asp Asp Pro Gln Arg Leu Gln Glu Leu
 85 90 95
 40 Thr Ala Ser Phe Asn Ala Glu Ser Glu Ala Trp Thr Glu Leu Ile Glu
 100 105 110
 45 Lys Ala Ser Lys Ser Val Gln Val Asp Tyr Val Gly Gly Thr Ile Ala
 115 120 125
 50 Gly Thr Ala Val Ala Ser Arg Gln Ile Gly Leu Leu Glu Leu Gln Ser
 130 135 140
 His Asp Ile Trp Glu His Trp Leu Arg Ser Arg Gly Leu Asn Ser Ser
 145 150 155 160
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Ser Phe Ala Arg Thr Lys Val Gln Ile
165

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<210> 20
<211> 713
<212> PRT
10 <213> Escherichia coli
<400> 20

Met Ala Met Phe Thr Pro Ser Phe Ser Gly Leu Lys Gly Arg Ala Leu
1 5 10 15

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Phe Ser Leu Leu Phe Ala Ala Pro Met Ile His Ala Thr Asp Ser Val
26 25 30

20

Thr Thr Lys Asp Gly Glu Thr Ile Thr Val Thr Ala Asp Ala Asn Thr
35 40 45

25

Ala Thr Glu Ala Thr Asp Gly Tyr Gln Pro Leu Ser Thr Ser Thr Ala
50 55 60

30

Thr Leu Thr Asp Met Pro Met Leu Asp Ile Pro Gln Val Val Asn Thr
65 70 75 80

Val Ser Asp Gln Val Leu Glu Asn Gln Asn Ala Thr Thr Leu Asp Glu
85 90 95

35

Ala Leu Tyr Asn Val Ser Asn Val Val Gln Thr Asn Thr Leu Gly Gly
100 105 110

40

Thr Gln Asp Ala Phe Val Arg Arg Gly Phe Gly Ala Asn Arg Asp Gly
115 120 125

45

Ser Ile Met Thr Asn Gly Leu Arg Thr Val Leu Pro Arg Ser Phe Asn
130 135 140

Ala Ala Thr Glu Arg Val Glu Val Leu Lys Gly Pro Ala Ser Thr Leu
145 150 155 160

50

Tyr Gly Ile Leu Asp Pro Gly Gly Leu Ile Asn Val Val Thr Lys Arg
165 170 175

Pro Glu Lys Thr Phe His Gly Ser Val Ser Ala Thr Ser Ser Phe

55

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180 185 190

5 Gly Gly Gly Thr Gly Gln Leu Asp Ile Thr Gly Pro Ile Glu Gly Thr
195 200 205

10 Gln Leu Ala Tyr Arg Leu Thr Gly Glu Val Gln Asp Glu Asp Tyr Trp
210 215 220

15 Arg Asn Phe Gly Lys Glu Arg Ser Thr Phe Ile Ala Pro Ser Leu Thr
225 230 235 240

20 Trp Phe Gly Asp Asn Ala Thr Val Thr Met Leu Tyr Ser His Arg Asp
245 250 255

25 Tyr Lys Thr Pro Phe Asp Arg Gly Thr Ile Phe Asp Leu Thr Thr Lys
260 265 270

30 Gln Pro Val Asn Val Asp Arg Lys Ile Arg Phe Asp Glu Pro Phe Asn
275 280 285

35 Ile Thr Asp Gly Gln Ser Asp Leu Ala Gln Leu Asn Ala Glu Tyr His
290 295 300

40 Leu Asn Ser Gln Trp Thr Ala Arg Phe Asp Tyr Ser Tyr Ser Gln Asp
305 310 315 320

45 Lys Tyr Ser Asp Asn Gln Ala Arg Val Thr Ala Tyr Asp Ala Thr Thr
325 330 335

50 Gly Thr Leu Thr Arg Arg Val Asp Ala Thr Gln Gly Ser Thr Gln Arg
340 345 350

55 Met His Ala Thr Arg Ala Asp Leu Gln Gly Asn Val Asp Ile Ala Gly
355 360 365

60 Phe Tyr Asn Glu Ile Leu Gly Gly Val Ser Tyr Glu Tyr Tyr Asp Leu
370 375 380

65 Leu Arg Thr Asp Met Ile Arg Cys Lys Lys Ala Lys Asp Phe Asn Ile
385 390 395 400

70 Tyr Asn Pro Val Tyr Gly Asn Thr Ser Lys Cys Thr Thr Val Ser Ala
405 410 415

5

Ser Asp Ser Asp Gln Thr Ile Lys Gln Glu Asn Tyr Ser Ala Tyr Ala
 420 425 430

10

Gln Asp Ala Leu Tyr Leu Thr Asp Asn Trp Ile Ala Val Ala Gly Ile
 435 440 445

15

Arg Tyr Gln Tyr Tyr Thr Gln Tyr Ala Gly Lys Gly Arg Pro Phe Asn
 450 455 460

20

Val Asn Thr Asp Ser Arg Asp Glu Gln Trp Thr Pro Lys Leu Gly Leu
 465 470 475 480

25

Val Tyr Lys Leu Thr Pro Ser Val Ser Leu Phe Ala Asn Tyr Ser Gln
 485 490 495

30

Thr Phe Met Pro Gln Ser Ser Ile Ala Ser Tyr Ile Gly Asp Leu Pro
 500 505 510

35

Pro Glu Ser Ser Asn Ala Tyr Glu Val Gly Ala Lys Phe Glu Leu Phe
 515 520 525

40

Asp Gly Ile Thr Ala Asp Ile Ala Leu Phe Asp Ile His Lys Arg Asn
 530 535 540

45

Val Leu Tyr Thr Glu Ser Ile Gly Asp Glu Thr Ile Ala Lys Thr Ala
 545 550 555 560

50

Gly Arg Val Arg Ser Arg Gly Val Glu Val Asp Leu Ala Gly Ala Leu
 565 570 575

55

Thr Glu Asn Ile Asn Ile Ile Ala Ser Tyr Gly Tyr Thr Asp Ala Lys
 580 585 590

60

Val Leu Glu Asp Pro Asp Tyr Ala Gly Lys Pro Leu Pro Asn Val Pro
 595 600 605

65

Arg His Thr Gly Ser Leu Phe Leu Thr Tyr Asp Ile His Asn Met Pro
 610 615 620

70

Gly Asn Asn Thr Leu Thr Phe Gly Gly Gly His Gly Val Ser Arg
 625 630 635 640

75

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Arg Ser Ala Thr Asn Gly Ala Asp Tyr Tyr Leu Pro Gly Tyr Phe Val
645 650 655

5 Ala Asp Ala Phe Ala Ala Tyr Lys Met Lys Leu Gln Tyr Pro Val Thr
660 665 670

10 Leu Gln Leu Asn Val Lys Asn Leu Phe Asp Lys Thr Tyr Tyr Thr Ser
675 680 685

15 Ser Ile Ala Thr Asn Asn Leu Gly Asn Gln Ile Gly Asp Pro Arg Glu
690 695 700

20 Val Gln Phe Thr Val Lys Met Glu Phe
705 710

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<212> PRT
<213> Escherichia coli
<400> 21
Met Lys Ile Ser Trp Asn Tyr Ile Phe Lys Asn Lys Trp Arg Phe His
1 5 10 15

30 Ile Thr Ser Ile Ser Leu Phe Leu Ile Met Leu Ala Val Ser Ile Ala
20 25 30

35 Phe Leu His Leu Arg Phe Asn Thr Leu Ser Ser Thr Asp Lys Met Arg
35 40 45

40 Leu Glu Met Tyr Lys Ser Thr Leu Tyr Ser Thr Ile Glu Gln Phe Tyr
50 55 60

45 Val Leu Pro Tyr Met Leu Ser Thr Asp His Ile Ile Arg Gln Ala Val
65 70 75 80

50 Ile Thr Pro Asp Asp Met Thr Ser Ser Glu Leu Asn Gln Arg Ile Ala
85 90 95

His Phe Asn Thr Gln Leu Lys Thr Ala Ala Ile Phe Ile Leu Asp Thr
100 105 110

55 Gln Gly Lys Ala Ile Ala Ser Ser Asn Trp Gln Asp Pro Gly Ser Tyr
115 120 125

5

Val Gly Gln Asn Tyr Ser Tyr Arg Pro Tyr Tyr Lys His Ala Met Ser
 130 135 140

Gly Leu Asn Gly Arg Phe Tyr Gly Ile Gly Ser Thr Thr Asn Thr Pro
 145 150 155 160

10

Gly Phe Phe Leu Ser Thr Ser Ile Lys Asp Lys Gly Lys Ile Val Gly
 165 170 175

15

Val Val Val Val Lys Ile Ser Leu Asn Glu Ile Glu Lys Ala Trp Ala
 180 185 190

20

Glu Gly Pro Glu Asn Ile Ile Val Asn Asp Glu His Gly Ile Ile Phe
 195 200 205

Leu Ser Ser Lys Ser Pro Trp Arg Met Arg Thr Leu Gln Pro Leu Pro
 210 215 220

25

Val Gln Ala Lys Gln Lys Leu Gln Ser Thr Arg Gln Tyr Ser Leu Asp
 225 230 235 240

30

Asn Leu Leu Pro Ala Asp Tyr Tyr Pro Cys Tyr Thr Val Ser Asn Phe
 245 250 255

35

Thr Phe Leu Lys Asp Lys Lys Glu Gln Leu Cys Leu Phe Pro Gln Tyr
 260 265 270

Tyr Thr Gln Gln Ile Ala Ile Pro Glu Phe Asn Trp Lys Met Thr Ile
 275 280 285

40

Met Val Pro Leu Asp Asn Leu Tyr Trp Ser Trp Ala Ile Ser Leu Val
 290 295 300

45

Ile Thr Leu Ile Ile Tyr Leu Leu Phe Leu Leu Phe Ile Lys Tyr Trp
 305 310 315 320

Arg Met Arg Ser His Ala Gln Gln Leu Leu Thr Leu Ala Asn Glu Thr
 325 330 335

50

Leu Glu Lys Gln Val Lys Glu Arg Thr Ser Ala Leu Glu Leu Ile Asn
 340 345 350

55

Gln Lys Leu Ile Gln Glu Ile Lys Glu Arg Ser Gln Ala Glu Gln Val
 355 360 365

5 Leu Gln Ile Thr Arg Ser Glu Leu Ala Glu Ser Ser Lys Leu Ala Ala
 370 375 380

10 Leu Gly Gln Met Ala Thr Glu Ile Ala His Glu Gln Asn Gln Pro Leu
 385 390 395 400

15 Ala Ala Ile His Ala Leu Thr Asp Asn Ala Arg Thr Met Leu Lys Lys
 405 410 415

Glu Met Tyr Pro Gln Val Glu Gln Asn Leu Lys His Ile Ile Ser Val
 420 425 430

20 Ile Glu Arg Met Thr Gln Leu Ile Ser Glu Leu Lys Ala Phe Ala Ser
 435 440 445

25 Arg His Arg Val Pro Lys Gly Ser Ala Asp Val Ile Lys Val Met Tyr
 450 455 460

30 Ser Ala Val Ala Leu Leu Asn His Ser Met Glu Lys Asn Asn Ile Glu
 465 470 475 480

Arg Arg Ile Lys Ala Pro Ser Met Pro Leu Phe Val Asn Cys Asp Glu
 485 490 495

35 Leu Gly Leu Glu Gln Ile Phe Ser Asn Leu Ile Ser Asn Ala Leu Asp
 500 505 510

40 Ser Met Glu Gly Ser Ser Tyr Lys Arg Leu Asp Ile Ala Ile Arg Gln
 515 520 525

45 Ala Asn Asn Lys Val Ile Ile Thr Ile Lys Asp Ser Gly Gly Phe
 530 535 540

Ala Pro Glu Val Val Asp Arg Ile Phe Glu Pro Phe Phe Thr Thr Lys
 545 550 555 560

50 Arg Arg Gly Met Gly Leu Gly Leu Ala Ile Val Ser Glu Ile Val Arg
 565 570 575

55

Asn Ser Asn Gly Ala Leu His Ala Ser Asn His Pro Glu Gly Gly Ala
 580 585 590

5 Val Met Thr Leu Thr Trp Pro Glu Trp Gly Glu Glu His Glu
 595 600 605

10 <210> 22
 <211> 101
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 <400> 22

15 Val Leu Thr Pro Gln His Leu Arg Cys Val Leu Thr Cys Ser Asp Leu
 1 5 10 15

20 Leu Thr Leu Leu Ser Gly Thr Val Met Ser Gln Met Pro Leu Tyr Phe
 20 25 30

25 Leu Asn Thr Gln Lys Lys Leu Thr Ala His Tyr Glu Trp Leu Gln Ile
 35 40 45

30 Asn Leu Thr Asp Thr Tyr Glu Leu Val Lys Arg Leu Met Pro Ile Pro
 50 55 60

35 Ser Leu Asp Val Val Lys Val Gly Lys Leu Val Leu Pro Glu Lys
 65 70 75 80

40 Gly His His Gly Phe Tyr Pro Glu Ala Gly Val Val Tyr Arg Thr Val
 85 90 95

35

Ala Pro Glu Asn Pro
 100

40

<210> 23
 <211> 263
 <212> PRT
 <213> Escherichia coli
 <400> 23

45

Met Met Lys Asn Thr Gly Tyr Ile Leu Ala Leu Cys Leu Thr Ala Ser
 1 5 10 15

50

Gly His Val Leu Ala His Asp Val Trp Ile Thr Gly Lys Gln Ala Glu
 20 25 30

55

Asn Asn Val Thr Ala Glu Ile Gly Tyr Gly His Asn Phe Pro Ser Lys

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40

5	Gly Thr Ile Pro Asp Arg Arg Asp Phe Phe Glu Asn Pro Arg Leu Tyr 50 55 60
10	Asn Gly Lys Glu Thr Ile Thr Leu Lys Pro Ala Ser Thr Asp Tyr Val 65 70 75 80
15	Tyr Lys Thr Glu Ser Ala Ser Lys Asp Asn Gly Tyr Val Leu Ser Thr 85 90 95
20	Tyr Met Lys Pro Gly Tyr Trp Ser Arg Thr Ser Ser Gly Trp Lys Pro 100 105 110
25	Val Ser Arg Glu Gly Arg Asn Asp Val Ala Tyr Cys Glu Phe Val Thr 115 120 125
30	Lys Tyr Ala Lys Ser Phe Ile Pro Gly Glu Gln Gln Met Pro Ala Gln 130 135 140
35	Leu Tyr Gln Ser Pro Thr Gly His Glu Leu Glu Ile Ile Pro Leu Ser 145 150 155 160
40	Asp Ile Ser Arg Phe Ser Glu Asn Val Lys Leu Lys Val Leu Tyr Lys 165 170 175
45	Thr Ser Pro Leu Ala Gly Ala Ile Met Glu Leu Asp Ser Val Ser Tyr 180 185 190
50	Leu Thr Ser Ser Arg His Thr His Ala Val Glu His Lys His Pro Val 195 200 205
	His Lys Ala Glu Leu Thr Phe Val Thr Asn Glu Asp Gly Ile Val Thr 210 215 220
	Val Pro Ser Leu His Ile Gly Gln Trp Leu Ala Lys Val Gln Asn Lys 225 230 235 240
	Lys Ser Phe Gln Asp Lys Ser Leu Cys Asp Glu Thr Val Asp Val Ala 245 250 255
	Thr Leu Ser Phe Ser Arg Asn 260

5 <210> 24
 <211> 378
 <212> PRT
 <213> Escherichia coli
 <400> 24

10 Met Gly Lys Ile Lys Tyr Trp Leu Ile Val Gly Phe Ile Ile Leu Phe
 1 5 10 15

15 Ala Ile Phe Tyr Ile Ala Ile Ser Asp Arg Asp Ser Thr Leu Ser Arg
 20 25 30

15 Leu Lys Ser Ala Gly Glu Asn Gly Asp Val Glu Ala Gln Tyr Ala Leu
 35 40 45

20 Gly Leu Met Tyr Leu Tyr Gly Glu Ile Leu Asp Val Asp Tyr Gln Gln
 50 55 60

25 Ala Lys Ile Trp Tyr Glu Lys Ala Ala Asp Gln Asn Asp Pro Arg Ala
 65 70 75 80

30 Gln Ala Lys Leu Gly Val Met Tyr Ala Asn Gly Leu Gly Val Asn Gln
 85 90 95

30 Asp Tyr Gln Gln Ser Lys Leu Trp Tyr Glu Lys Ala Ala Ala Gln Asn
 100 105 110

35 Asp Val Asp Ala Gln Phe Leu Leu Gly Glu Met Tyr Asp Asp Gly Leu
 115 120 125

40 Gly Val Ser Gln Asp Tyr Gln His Ala Lys Met Trp Tyr Glu Lys Ala
 130 135 140

40 Ala Ala Gln Asn Asp Glu Arg Ala Gln Val Asn Leu Ala Val Leu Tyr
 145 150 155 160

45 Ala Lys Gly Asn Gly Val Glu Gln Asp Tyr Arg Gln Ala Lys Ser Trp
 165 170 175

50 Tyr Glu Lys Ala Ala Ala Gln Asn Ser Pro Asp Ala Gln Phe Ala Leu
 180 185 190

55 Gly Ile Leu Tyr Ala Asn Ala Asn Gly Val Glu Gln Asp Tyr Gln Gln

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195 200 205

Ala Lys Asp Trp Tyr Glu Lys Ala Ala Glu Gln Asn Phe Ala Asn Ala
210 215 220

Gln Phe Asn Leu Gly Met Leu Tyr Tyr Lys Gly Glu Gly Val Lys Gln
 225 230 235 240

10 Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn
Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn
245 250 255

15 Gln Pro Asn Ala Gln Tyr Asn Leu Gly Gln Ile Tyr Tyr Tyr Gly Gln
 260 265 270

20 Gly Val Thr Gln Ser Tyr Arg Gln Ala Lys Asp Trp Phe Glu Lys Ala
 275 280 285

Ala Glu Lys Gly His Val Asp Ala Gln Tyr Asn Leu Gly Val Ile Tyr
290 295 300

25 Glu Asn Gly Glu Gly Val Ser Gln Asn Tyr Gln Gln Ala Lys Ala Trp
305 310 315 320

35 Gly Val Met Asn Glu Leu Gly Gln Gly Glu Ser Ile Asp Leu Lys Gln
340 345 350

Ala Arg His Tyr Tyr Glu Arg Ser Cys Asn Asn Gly Leu Lys Lys Gly
355 360 365

40 Cys Glu Arg Leu Lys Glu Leu Leu Tyr Lys
370 375

45 <210> 25
<211> 654
<212> PRT
<213> Escherichia coli
<400> 25

50 Met Asn Val Ile Arg Thr Val Ile Cys Thr Leu Ile Ile Leu Pro Val
1 5 10 15

Gly Leu Gln Ala Ala Thr Ser His Ser Ser Met Val Lys Asp Thr Ile
 20 25 30

5 Thr Ile Val Ala Thr Gly Asn Gln Asn Thr Val Phe Glu Thr Pro Ser
 35 40 45

10 Met Val Ser Val Val Thr Asn Asp Thr Pro Trp Ser Gln Asn Ala Val
 50 55 60

15 Thr Ser Ala Gly Met Leu Lys Gly Val Ala Gly Leu Ser Gln Thr Gly
 65 70 75 80

Ala Gly Arg Thr Asn Gly Gln Thr Phe Asn Leu Arg Gly Tyr Asp Lys
 85 90 95

20 Ser Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Leu Ser Asp Met
 100 105 110

25 Ala Lys Ser Ser Gly Thr Tyr Leu Asp Pro Ala Leu Val Lys Arg Ile
 115 120 125

30 Glu Val Val Arg Gly Pro Asn Ser Ser Leu Tyr Gly Ser Gly Gly Leu
 130 135 140

35 Pro Gly Glu Thr Asn Gly Leu Ser Leu Trp Gly Asn Ile Ala Ser Gly
 145 150 155 160

40 Asp His Ser Thr Gly Ser Gly Leu Thr Trp Phe Gly Lys Thr Gly Lys
 180 185 190

45 Thr Asp Ala Leu Leu Ser Val Ile Met Arg Lys Arg Gly Asn Ile Tyr
 195 200 205

Gln Ser Asp Gly Glu His Ala Pro Asn Lys Glu Lys Pro Ala Ala Leu
 210 215 220

50 Phe Ala Lys Gly Ser Val Gly Ile Thr Asp Ser Asn Lys Ala Gly Ala
 225 230 235 240

55 Ser Leu Arg Leu Tyr Arg Asn Asn Thr Thr Glu Pro Gly Asn Ser Thr

	245	250	255
5	Gln Thr His Gly Asp Ser Gly Leu Arg Asp Arg Lys Thr Val Gln Asn 260	265	270
10	Asp Val Gln Phe Trp Tyr Gln Tyr Ala Pro Val Asp Asn Ser Leu Ile 275	280	285
15	Asn Val Lys Ser Thr Leu Tyr Leu Ser Asp Ile Thr Ile Lys Thr Asn 290	295	300
20	Gly His Asn Lys Thr Ala Glu Trp Arg Asn Asn Arg Thr Ser Gly Val 305	310	315
25	Asn Val Val Asn Arg Ser His Thr Leu Ile Phe Pro Gly Ala His Gln 325	330	335
30	Leu Ser Tyr Gly Ala Glu Tyr Tyr Arg Gln Gln Gln Lys Pro Glu Gly 340	345	350
35	Ser Ala Thr Leu Tyr Pro Glu Gly Asn Ile Asp Phe Thr Ser Leu Tyr 355	360	365
40	Phe Gln Asp Glu Met Thr Met Lys Ser Tyr Pro Val Asn Ile Ile Val 370	375	380
45	Gly Ser Arg Tyr Asp Arg Tyr Lys Ser Phe Asn Pro Arg Ala Gly Glu 385	390	395
50	Leu Lys Ala Glu Arg Leu Ser Pro Arg Ala Ala Ile Ser Val Ser Pro 405	410	415
55	Thr Asp Trp Leu Met Met Tyr Gly Ser Ile Ser Ser Ala Phe Arg Ala 420	425	430
	Pro Thr Met Ala Glu Met Tyr Arg Asp Asp Val His Phe Tyr Arg Lys 435	440	445
	Gly Lys Pro Asn Tyr Trp Val Pro Asn Leu Asn Leu Lys Pro Glu Asn 450	455	460
	Asn Ile Thr Arg Glu Ile Gly Ala Gly Ile Gln Leu Asp Gly Leu Leu 465	470	475

5 Thr Asp Asn Asp Arg Leu Gln Leu Lys Gly Gly Tyr Phe Gly Thr Asp
485 490 495

10 Ala Arg Asn Tyr Ile Ala Thr Arg Val Asp Met Lys Arg Met Arg Ser
500 505 510

15 Tyr Ser Tyr Asn Val Ser Arg Ala Arg Ile Trp Gly Trp Asp Met Gln
515 520 525

20 Gly Asn Tyr Gln Ser Asp Tyr Val Asp Trp Met Leu Ser Tyr Asn Arg
530 535 540

25 Thr Glu Ser Met Asp Ala Ser Ser Arg Glu Trp Leu Gly Ser Gly Asn
545 550 555 560

30 Pro Asp Thr Leu Ile Ser Asp Ile Ser Ile Pro Val Gly His Arg Gly
565 570 575

35 Val Tyr Ala Gly Trp Arg Ala Glu Leu Ser Ala Ser Ala Thr His Val
580 585 590

40 Lys Lys Gly Asp Pro His Gln Ala Gly Tyr Thr Ile His Ser Phe Ser
595 600 605

45 Leu Ser Tyr Lys Pro Val Ser Val Lys Gly Phe Glu Ala Ser Val Thr
610 615 620

50 Leu Asp Asn Ala Phe Asn Lys Leu Ala Met Asn Gly Lys Gly Val Pro
625 630 635 640

55 Leu Ser Gly Arg Thr Val Ser Leu Tyr Thr Arg Tyr Gln Trp
645 650

45 <210> 26

<211> 1376

<212> PRT

<213> Escherichia coli

<400> 26

50 Met Asn Lys Ile Tyr Ala Leu Lys Tyr Cys Tyr Ile Thr Asn Thr Val
1 5 10 15

55 Lys Val Val Ser Glu Leu Ala Arg Arg Val Cys Lys Gly Ser Thr Arg

5	20	25	30
	Arg Gly Lys Arg Leu Ser Val Leu Thr Ser Leu Ala Leu Ser Ala Leu 35	40	45
10	Leu Pro Thr Val Ala Gly Ala Ser Thr Val Gly Gly Asn Asn Pro Tyr 50	55	60
	Gln Thr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Gln Phe Gln Ala Gly 65	70	75
15	Ala Thr Asn Ile Pro Ile Phe Asn Asn Lys Gly Glu Leu Val Gly His 85	90	95
20	Leu Asp Lys Ala Pro Met Val Asp Phe Ser Ser Val Asn Val Ser Ser 100	105	110
25	Asn Pro Gly Val Ala Thr Leu Ile Asn Pro Gln Tyr Ile Ala Ser Val 115	120	125
	Lys His Asn Lys Gly Tyr Gln Ser Val Ser Phe Gly Asp Gly Gln Asn 130	135	140
30	Ser Tyr His Ile Val Asp Arg Asn Glu His Ser Ser Ser Asp Leu His 145	150	155
35	Thr Pro Arg Leu Asp Lys Leu Val Thr Glu Val Ala Pro Ala Thr Val 165	170	175
	Thr Ser Ser Ser Thr Ala Asp Ile Leu Asn Pro Ser Lys Tyr Ser Ala 180	185	190
40	Phe Tyr Arg Ala Gly Ser Gly Ser Gln Tyr Ile Gln Asp Ser Gln Gly 195	200	205
45	Lys Arg His Trp Val Thr Gly Gly Tyr Gly Tyr Leu Thr Gly Gly Ile 210	215	220
50	Leu Pro Thr Ser Phe Phe Tyr His Gly Ser Asp Gly Ile Gln Leu Tyr 225	230	240
	Met Gly Gly Asn Ile His Asp His Ser Ile Leu Pro Ser Phe Gly Glu 245	250	255

5

Ala Gly Asp Ser Gly Ser Pro Leu Phe Gly Trp Asn Thr Ala Lys Gly
 260 265 270

10

Gln Trp Glu Leu Val Gly Val Tyr Ser Gly Val Gly Gly Thr Asn
 275 280 285

20

Leu Ile Tyr Ser Leu Ile Pro Gln Ser Phe Leu Ser Gln Ile Tyr Ser
 290 295 300

Glu Asp Asn Asp Ala Pro Val Phe Phe Asn Ala Ser Ser Gly Ala Pro
 305 310 315 320

Leu Gln Trp Lys Phe Asp Ser Ser Thr Gly Thr Gly Ser Leu Lys Gln
 325 330 335

25

Gly Ser Asp Glu Tyr Ala Met His Gly Gln Lys Gly Ser Asp Leu Asn
 340 345 350

Ala Gly Lys Asn Leu Thr Phe Leu Gly His Asn Gly Gln Ile Asp Leu
 355 360 365

30

Glu Asn Ser Val Thr Gln Gly Ala Gly Ser Leu Thr Phe Thr Asp Asp
 370 375 380

35

Tyr Thr Val Thr Thr Ser Asn Gly Ser Thr Trp Thr Gly Ala Gly Ile
 385 390 395 400

Ile Val Asp Lys Asp Ala Ser Val Asn Trp Gln Val Asn Gly Val Lys
 405 410 415

40

Gly Asp Asn Leu His Lys Ile Gly Glu Gly Thr Leu Val Val Gln Gly
 420 425 430

45

Thr Gly Val Asn Glu Gly Leu Lys Val Gly Asp Gly Thr Val Val
 435 440 445

50

Leu Asn Gln Gln Ala Asp Ser Ser Gly His Val Gln Ala Phe Ser Ser
 450 455 460

Val Asn Ile Ala Ser Gly Arg Pro Thr Val Val Leu Ala Asp Asn Gln
 465 470 475 480

55

Gln Val Asn Pro Asp Asn Ile Ser Trp Gly Tyr Arg Gly Gly Val Leu
 485 490 495

5 Asp Val Asn Gly Asn Asp Leu Thr Phe His Lys Leu Asn Ala Ala Asp
 500 505 510

10 Tyr Gly Ala Thr Leu Gly Asn Ser Ser Asp Lys Thr Ala Asn Ile Thr
 515 520 525

15 Leu Asp Tyr Gln Thr Arg Pro Ala Asp Val Lys Val Asn Glu Trp Ser
 530 535 540

Ser Ser Asn Arg Gly Thr Val Gly Ser Leu Tyr Ile Tyr Asn Asn Pro
 545 550 555 560

20 Tyr Thr His Thr Val Asp Tyr Phe Ile Leu Lys Thr Ser Ser Tyr Gly
 565 570 575

25 Trp Phe Pro Thr Gly Gln Val Ser Asn Glu His Trp Glu Tyr Val Gly
 580 585 590

30 His Asp Gln Asn Ser Ala Gln Ala Leu Leu Ala Asn Arg Ile Asn Asn
 595 600 605

Lys Gly Tyr Leu Tyr His Gly Lys Leu Leu Gly Asn Ile Asn Phe Ser
 610 615 620

35 Asn Lys Ala Thr Pro Gly Thr Thr Gly Ala Leu Val Met Asp Gly Ser
 625 630 635 640

40 Ala Asn Met Ser Gly Thr Phe Thr Gln Glu Asn Gly Arg Leu Thr Ile
 645 650 655

45 Gln Gly His Pro Val Ile His Ala Ser Thr Ser Gln Ser Ile Ala Asn
 660 665 670

Thr Val Ser Ser Leu Gly Asp Asn Ser Val Leu Thr Gln Pro Thr Ser
 675 680 685

50 Phe Thr Gln Asp Asp Trp Glu Asn Arg Thr Phe Ser Phe Gly Ser Leu
 690 695 700

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Val Leu Lys Asp Thr Asp Phe Gly Leu Gly Arg Asn Ala Thr Leu Asn
 705 710 715 720

5 Thr Thr Ile Gln Ala Asp Asn Ser Ser Val Thr Leu Gly Asp Ser Arg
 725 730 735

10 Val Phe Ile Asp Lys Lys Asp Gly Gln Gly Thr Ala Phe Thr Leu Glu
 740 745 750

Glu Gly Thr Ser Val Ala Thr Lys Asp Ala Asp Lys Ser Val Phe Asn
 755 760 765

15 Gly Thr Val Asn Leu Asp Asn Gln Ser Val Leu Asn Ile Asn Glu Ile
 770 775 780

20 Phe Asn Gly Gly Ile Gln Ala Asn Asn Ser Thr Val Asn Ile Ser Ser
 785 790 795 800

25 Asp Ser Ala Val Leu Glu Asn Ser Thr Leu Thr Ser Thr Ala Leu Asn
 805 810 815

Leu Asn Lys Gly Ala Asn Val Leu Ala Ser Gln Ser Phe Val Ser Asp
 820 825 830

30 Gly Pro Val Asn Ile Ser Asp Ala Thr Leu Ser Leu Asn Ser Arg Pro
 835 840 845

35 Asp Glu Val Ser His Thr Leu Leu Pro Val Tyr Asp Tyr Ala Gly Ser
 850 855 860

40 Trp Asn Leu Lys Gly Asp Asp Ala Arg Leu Asn Val Gly Pro Tyr Ser
 865 870 875 880

45 Met Leu Ser Gly Asn Ile Asn Val Gln Asp Lys Gly Thr Val Thr Leu
 885 890 895

Gly Gly Glu Gly Glu Leu Ser Pro Asp Leu Thr Leu Gln Asn Gln Met
 900 905 910

50 Leu Tyr Ser Leu Phe Asn Gly Tyr Arg Asn Thr Trp Ser Gly Ser Leu
 915 920 925

55 Asn Ala Pro Asp Ala Thr Val Ser Met Thr Asp Thr Gln Trp Ser Met

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930	935	940
5 945	Asn Gly Asn Ser Thr Ala Gly Asn Met Lys Leu Asn Arg Thr Ile Val 950	955 960
10 965	Gly Phe Asn Gly Gly Thr Ser Ser Phe Thr Thr Leu Thr Thr Asp Asn 970	975
15 995	Leu Asp Ala Val Gln Ser Ala Phe Val Met Arg Thr Asp Leu Asn Lys 985	990
20 1010	Ala Asp Lys Leu Val Ile Asn Lys Ser Ala Thr Gly His Asp Asn Ser 1000	1005
25 1025	Ile Trp Val Asn Phe Leu Lys Lys Pro Ser Asp Lys Asp Thr Leu 1015	1020
30 1055	Asp Ile Pro Leu Val Ser Ala Pro Glu Ala Thr Ala Asp Asn Leu 1030	1035
35 1070	Phe Arg Ala Ser Thr Arg Val Val Gly Phe Ser Asp Val Thr Pro 1040	1045
40 1085	Thr Leu Ser Val Arg Lys Glu Asp Gly Lys Lys Glu Trp Val Leu 1060	1065
45 1100	Asp Gly Tyr Gln Val Ala Arg Asn Asp Gly Gln Gly Lys Ala Ala 1075	1080
50 1115	Ala Thr Phe Met His Ile Ser Tyr Asn Asn Phe Ile Thr Glu Val 1090	1095
55 1130	Asn Asn Leu Asn Lys Arg Met Gly Asp Leu Arg Asp Ile Asn Gly 1105	1110
55 1145	Glu Ala Gly Thr Trp Val Arg Leu Leu Asn Gly Ser Gly Ser Ala 1120	1125
55 1150	Asp Gly Gly Phe Thr Asp His Tyr Thr Leu Leu Gln Met Gly Ala 1135	1140
55 1155	Asp Arg Lys His Glu Leu Gly Ser Met Asp Leu Phe Thr Gly Val 1145	1150

5 Met Ala Thr Tyr Thr Asp Thr Asp Ala Ser Ala Gly Leu Tyr Ser
1160 1165 1170

10 Gly Lys Thr Lys Ser Trp Gly Gly Gly Phe Tyr Ala Ser Gly Leu
1175 1180 1185

15 Phe Arg Ser Gly Ala Tyr Phe Asp Leu Ile Ala Lys Tyr Ile His
1190 1195 1200

20 Asn Glu Asn Lys Tyr Asp Leu Asn Phe Ala Gly Ala Gly Lys Gln
1205 1210 1215

25 Asn Phe Arg Ser His Ser Leu Tyr Ala Gly Ala Glu Val Gly Tyr
1220 1225 1230

30 Arg Tyr His Leu Thr Asp Thr Thr Phe Val Glu Pro Gln Ala Glu
1235 1240 1245

35 Leu Val Trp Gly Arg Leu Gln Gly Gln Thr Phe Asn Trp Asn Asp
1250 1255 1260

40 Ser Gly Met Asp Val Ser Met Arg Arg Asn Ser Val Asn Pro Leu
1265 1270 1275

45 Val Gly Arg Thr Gly Val Val Ser Gly Lys Thr Phe Ser Gly Lys
1280 1285 1290

50 Asp Trp Ser Leu Thr Ala Arg Ala Gly Leu His Tyr Glu Phe Asp
1295 1300 1305

55 Leu Thr Asp Ser Ala Asp Val His Leu Lys Asp Ala Ala Gly Glu
1310 1315 1320

His Gln Ile Asn Gly Arg Lys Asp Gly Arg Met Leu Tyr Gly Val
1325 1330 1335

Gly Leu Asn Ala Arg Phe Gly Asp Asn Thr Arg Leu Gly Leu Glu
1340 1345 1350

Val Glu Arg Ser Ala Phe Gly Lys Tyr Asn Thr Asp Asp Ala Ile
1355 1360 1365

Asn Ala Asn Ile Arg Tyr Ser Phe
 1370 1375
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 <211> 349
 <212> PRT
 <213> Escherichia coli
 10 <400> 27
 Met Ile Thr Leu Phe Arg Leu Leu Ala Ile Leu Cys Leu Phe Phe Asn
 1 5 10 15
 15 Val Ser Ala Phe Ala Val Asp Cys Tyr Gln Asp Gly Tyr Arg Gly Thr
 20 25 30
 20 Thr Leu Ile Asn Gly Asp Leu Pro Thr Phe Lys Ile Pro Glu Asn Ala
 35 40 45
 25 Gln Pro Gly Gln Lys Ile Trp Glu Ser Gly Asp Ile Asn Ile Thr Val
 50 55 60
 30 Tyr Cys Asp Asn Ala Pro Gly Trp Ser Ser Asn Asn Pro Ser Glu Asn
 65 70 75 80
 35 Val Tyr Ala Trp Ile Lys Leu Pro Gln Ile Asn Ser Ala Asp Met Leu
 85 90 95
 40 Asn Asn Pro Tyr Leu Thr Phe Gly Val Thr Tyr Asn Gly Val Asp Tyr
 100 105 110
 45 Glu Gly Thr Asn Glu Lys Ile Asp Thr His Ala Cys Leu Asp Lys Tyr
 115 120 125
 50 Glu Gln Tyr Tyr Asn Gly Tyr Tyr His Asp Pro Val Cys Asn Gly Ser
 130 135 140
 45 Thr Leu Gln Lys Asn Val Thr Phe Asn Ala His Phe Arg Val Tyr Val
 145 150 155 160
 50 Lys Phe Lys Ser Arg Pro Ala Gly Asp Gln Thr Val Asn Phe Gly Thr
 165 170 175
 55 Val Asn Val Leu Gln Phe Asp Gly Glu Gly Ala Asn Met Ala Pro
 180 185 190

5

Asn Ala Lys Asn Leu Arg Tyr Ala Ile Thr Gly Leu Asp Asn Ile Ser
 195 200 205

10

Phe Leu Asp Cys Ser Val Asp Val Arg Ile Ser Pro Glu Ser Gln Ile
 210 215 220

20

Val Asn Phe Gly Gln Ile Ala Ala Asn Ser Ile Ala Thr Phe Pro Pro
 225 230 235 240

15

Lys Ala Ala Phe Ser Val Ser Thr Ile Lys Asp Ile Ala Ser Asp Cys
 245 250 255

Thr Glu Gln Phe Asp Val Ala Thr Ser Phe Phe Thr Ser Asp Thr Leu
 260 265 270

Tyr Asp Asn Thr His Leu Glu Ile Gly Asn Gly Leu Leu Met Arg Ile
 275 280 285

25

Thr Asp Gln Lys Thr Gln Glu Asp Ile Lys Phe Asn Gln Phe Lys Leu
 290 295 300

30

Phe Ser Thr Tyr Ile Pro Gly Gln Ser Ala Ala Met Ala Thr Arg Asp
 305 310 315 320

35

Tyr Gln Ala Glu Leu Thr Gln Lys Pro Gly Glu Pro Leu Val Tyr Gly
 325 330 335

Pro Phe Gln Lys Asp Leu Ile Val Lys Ile Asn Tyr His
 340 345

40

<210> 28
 <211> 840
 <212> PRT
 <213> Escherichia coli
 <400> 28

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Met Asn Asn Lys Asn Thr Phe Ser Arg Asp Lys Leu Ser His Ala Ile
 1 5 10 15

50

Lys Asn Ala Leu Ser Gly Val Val Cys Ser Leu Leu Phe Val Leu Pro
 20 25 30

55

Val His Ala Val Glu Phe Asn Val Asp Met Ile Asp Ala Glu Asp Arg

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	35	40	45	
5	Glu Asn Ile Asp Ile Ser Arg Phe Glu Lys Lys Gly Tyr Ile Pro Pro 50	55	60	
10	Gly Arg Tyr Leu Val Arg Val Gln Ile Asn Lys Asn Met Leu Pro Gln 65	70	75	80
	Thr Leu Ile Leu Glu Trp Val Lys Ala Asp Asn Glu Ser Gly Ser Leu 85	90	95	
15	Leu Cys Leu Thr Lys Glu Asn Leu Thr Asn Phe Gly Leu Asn Thr Glu 100	105	110	
20	Phe Ile Glu Ser Leu Gln Asn Ile Ala Gly Ser Glu Cys Leu Asp Leu 115	120	125	
25	Ser Gln Arg Gln Glu Leu Thr Thr Arg Leu Asp Lys Ala Thr Met Ile 130	135	140	
	Leu Ser Leu Ser Val Pro Gln Ala Trp Leu Lys Tyr Gln Ala Thr Asn 145	150	155	160
30	Trp Thr Pro Pro Glu Phe Trp Asp Thr Gly Ile Thr Gly Phe Ile Leu 165	170	175	
35	Asp Tyr Asn Val Tyr Ala Ser Gln Tyr Ala Pro His His Gly Asp Ser 180	185	190	
40	Thr Gln Asn Val Ser Ser Tyr Gly Thr Leu Gly Phe Asn Leu Gly Ala 195	200	205	
	Trp Arg Leu Arg Ser Asp Tyr Gln Tyr Asn Gln Asn Phe Ala Asp Gly 210	215	220	
45	Arg Ser Val Asn Arg Asp Ser Glu Phe Ala Arg Thr Tyr Leu Phe Arg 225	230	235	240
50	Pro Ile Pro Ser Trp Ser Ser Lys Phe Thr Met Gly Gln Tyr Asp Leu 245	250	255	
55	Ser Ser Asn Leu Tyr Asp Thr Phe His Phe Thr Gly Ala Ser Leu Glu 260	265	270	

Lys Glu Ser Tyr Val Ile Ser Leu Asn Gln Tyr Phe Glu Thr Leu Glu
 500 505 510

5
 Leu Asn Ser Tyr Leu Asn Val Thr Arg Asn Thr Tyr Trp Asp Ser Ala
 515 520 525

10 Ser Asn Thr Asn Tyr Ser Val Ser Val Ser Lys Asn Phe Asp Ile Gly
 530 535 540

15 Asp Phe Lys Gly Ile Ser Ala Ser Leu Ala Val Ser Arg Ile Arg Trp
 545 550 555 560

Asp Asp Asp Glu Glu Asn Gln Tyr Tyr Phe Ser Phe Ser Leu Pro Leu
 565 570 575

20 Gln Gln Asn Arg Asn Ile Ser Tyr Ser Met Gln Arg Thr Gly Ser Ser
 580 585 590

25 Asn Thr Ser Gln Met Ile Ser Trp Tyr Asp Ser Ser Asp Arg Asn Asn
 595 600 605

30 Ile Trp Asn Ile Ser Ala Ser Ala Thr Asp Asp Asn Ile Arg Asp Gly
 610 615 620

Glu Pro Thr Leu Arg Gly Ser Tyr Gln His Tyr Ser Pro Trp Gly Arg
 625 630 635 640

35 Leu Asn Ile Asn Gly Ser Val Gln Pro Asn Gln Tyr Asn Ser Val Thr
 645 650 655

40 Ala Gly Trp Tyr Gly Ser Leu Thr Ala Thr Arg His Gly Val Ala Leu
 660 665 670

45 His Asp Tyr Ser Tyr Gly Asp Asn Ala Arg Met Met Val Asp Thr Asp
 675 680 685

50 Gly Ile Ser Gly Ile Glu Ile Asn Ser Asn Arg Thr Val Thr Asn Gly
 690 695 700 705

55 Leu Gly Ile Ala Val Ile Pro Ser Leu Ser Asn Tyr Thr Thr Ser Met
 710 715 720

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Leu Arg Val Asn Asn Asn Asp Leu Pro Glu Gly Val Asp Val Glu Asn
 725 730 735

5 Ser Val Ile Arg Thr Thr Leu Thr Gln Gly Ala Ile Gly Tyr Ala Lys
 740 745 750

10 Leu Asn Ala Thr Thr Gly Tyr Gln Ile Val Gly Val Ile Arg Gln Glu
 755 760 765

15 Asn Gly Arg Phe Pro Pro Leu Gly Val Asn Val Thr Asp Lys Ala Thr
 770 775 780

Gly Lys Asp Val Gly Leu Val Ala Glu Asp Gly Phe Val Tyr Leu Ser
 785 790 795 800

20 Gly Ile Gln Glu Asn Ser Ile Leu His Leu Thr Trp Gly Asp Asn Thr
 805 810 815

25 Cys Glu Val Thr Pro Pro Asn Gln Ser Asn Ile Ser Glu Ser Ala Ile
 820 825 830

Ile Leu Pro Cys Lys Thr Val Lys
 835 840

30
 <210> 29
 <211> 169
 <212> PR'T
 35 <213> Escherichia coli
 <400> 29

Leu Met Asn Thr Lys Gln Ser Val Ala Gln Leu Ala Val Pro His Arg
 1 5 10 15

40 Lys Arg Leu Ser Ser Thr Met Val Val Ala Leu Leu Cys Val Val
 20 25 30

45 Ala Gly Ala Val Met Ile Asn Ala Ala Asp Phe Pro Ala Thr Ala Ile
 35 40 45

50 Glu Thr Asp Pro Gly Ala Ser Ala Phe Pro Thr Phe Tyr Ala Cys Ala
 50 55 60

Leu Ile Val Leu Ala Val Leu Leu Val Ile Arg Asp Leu Leu Gln Ala
 65 70 75 80

55

Lys Pro Ala Ser Cys Ala Asn Ala Gln Glu Lys Pro Ala Phe Arg Lys
 85 90 95

5
 Thr Ala Thr Gly Ile Ala Ala Thr Ala Phe Tyr Ile Val Ala Met Ser
 100 105 110

10
 Tyr Cys Gly Tyr Leu Ile Thr Thr Pro Val Phe Leu Ile Val Ile Met
 115 120 125

15
 Thr Leu Met Gly Tyr Arg Arg Trp Val Leu Thr Pro Gly Ile Ala Leu
 130 135 140

Leu Leu Thr Ala Ile Leu Trp Leu Leu Phe Val Glu Ala Leu Gln Val
 145 150 155 160

20
 Pro Leu Pro Val Gly Thr Phe Phe Glu
 165

25
 <210> 30
 <211> 311
 <212> PRT
 <213> Escherichia coli
 <400> 30

30
 Met Val Leu Leu Ala Gly Ala Ala Leu Ser Ile Ala Pro Val Gln Ala
 1 5 10 15

35
 Ala Ser Tyr Pro Thr Lys Gln Ile Glu Leu Val Val Pro Tyr Ala Ala
 20 25 30

Gly Gly Gly Thr Asp Leu Val Ala Arg Ala Phe Ala Asp Ala Ala Lys
 35 40 45

40
 Asn His Leu Pro Val Ser Ile Gly Val Ile Asn Lys Pro Gly Gly Gly
 50 55 60

45
 Gly Ala Ile Gly Leu Ser Glu Ile Ala Ala Ala Arg Pro Asn Gly Tyr
 65 70 75 80

50
 Lys Ile Gly Leu Gly Thr Val Glu Leu Thr Thr Leu Pro Ser Leu Gly
 85 90 95

Met Val Arg Phe Lys Thr Ser Asp Phe Lys Pro Ile Ala Arg Leu Asn
 100 105 110

55

5

Ala Asp Pro Ala Ala Ile Thr Val Arg Ala Asp Ala Pro Trp Asn Ser
 115 120 125

10

Tyr Glu Glu Phe Met Ala Tyr Ser Lys Ala Asn Pro Gly Lys Val Arg
 130 135 140

15

Ile Gly Asn Ser Gly Thr Gly Ala Ile Trp His Leu Ala Ala Ala Ala
 145 150 155 160

15

Leu Glu Asp Lys Thr Gly Thr Lys Phe Ser His Val Pro Tyr Asp Gly
 165 170 175

20

Ala Ala Pro Ala Ile Thr Gly Leu Leu Gly Gly His Ile Glu Ala Val
 180 185 190

25

Ser Val Ser Pro Gly Glu Val Ile Asn His Val Asn Gly Gly Lys Leu
 195 200 205

35

Lys Thr Leu Val Val Met Ala Asp Glu Arg Met Lys Thr Met Pro Asp
 210 215 220

30

Val Pro Thr Leu Lys Glu Lys Gly Val Asp Leu Ser Ile Gly Thr Trp
 225 230 235 240

35

Arg Gly Leu Ile Val Ser Gln Lys Thr Pro Gln Asp Val Val Asp Val
 245 250 255

40

Leu Ala Lys Ala Ala Lys Glu Thr Ala Glu Glu Pro Ala Phe Gln Asp
 260 265 270

45

Ala Leu Gln Lys Leu Asn Leu Asn Tyr Ala Trp Leu Asp Ala Ala Ser
 275 280 285

50

Phe Gln Thr Gln Ile Ser Glu Gln Glu Lys Tyr Phe Asp Glu Leu Leu
 290 295 300

Thr Arg Leu Gly Leu Lys Lys
 305 310

55

<210> 31
 <211> 722
 <212> PRT

<213> Escherichia coli
 <400> 31

5 Met Leu Arg Trp Lys Arg Cys Ile Ile Leu Thr Phe Ile Ser Gly Ala
 1 5 10 15

10 Ala Phe Ala Ala Pro Glu Ile Asn Val Lys Gln Asn Glu Ser Leu Pro
 20 25 30

15 Asp Leu Gly Ser Gln Ala Ala Gln Gln Asp Glu Gln Thr Asn Lys Gly
 35 40 45

20 Lys Ser Leu Lys Glu Arg Gly Ala Asp Tyr Val Ile Asn Ser Ala Thr
 50 55 60

25 Gln Gly Phe Glu Asn Leu Thr Pro Glu Ala Leu Glu Ser Gln Ala Arg
 65 70 75 80

30 Ser Tyr Leu Gln Ser Gln Ile Thr Ser Thr Ala Gln Ser Tyr Ile Glu
 85 90 95

35 Asp Thr Leu Ser Pro Tyr Gly Lys Val Arg Leu Asn Leu Ser Ile Gly
 100 105 110

40 Gln Gly Gly Asp Leu Asp Gly Ser Ser Ile Asp Tyr Phe Val Pro Trp
 115 120 125

45 Tyr Asp Asn Gln Thr Thr Val Tyr Phe Ser Gln Phe Ser Ala Gln Arg
 130 135 140

50 Lys Glu Asp Arg Thr Ile Gly Asn Ile Gly Leu Gly Val Arg Tyr Asn
 145 150 155 160

55 Phe Asp Lys Tyr Leu Leu Gly Asn Ile Phe Tyr Asp Tyr Asp Phe
 165 170 175

60 Thr Arg Gly His Arg Arg Leu Gly Leu Gly Ala Glu Ala Trp Thr Asp
 180 185 190

65 Tyr Leu Lys Phe Ser Gly Asn Tyr Tyr His Pro Leu Ser Asp Trp Lys
 195 200 205

70 Asp Ser Glu Asp Phe Asp Phe Tyr Glu Glu Arg Pro Ala Arg Gly Trp
 210 215 220

75

Asp Ile Arg Ala Glu Val Trp Leu Pro Ser Tyr Pro Gln Leu Gly Gly
 5 225 . 230 235 240
 Lys Ile Val Phe Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Gly
 10 245 . 250 255
 Thr Asp Asn Leu Glu Lys Asp Pro Tyr Ala Val Thr Leu Gly Leu Asn
 15 260 . 265 270
 Tyr Gln Pro Val Pro Leu Leu Thr Val Gly Thr Asp Tyr Lys Ala Gly
 20 275 . 280 285
 Thr Gly Asp Asn Ser Asp Val Ser Ile Asn Ala Thr Leu Asn Tyr Gln
 25 290 . 295 300
 Phe Gly Val Pro Leu Lys Asp Gln Leu Asp Ser Asp Lys Val Lys Ala
 30 305 . 310 315 320
 Ala His Ser Leu Met Gly Ser Arg Leu Asp Phe Val Glu Arg Asn Asn
 35 325 . 330 335
 Phe Ile Val Leu Glu Tyr Lys Glu Lys Asp Pro Leu Asp Val Thr Leu
 40 340 . 345 350
 Trp Leu Lys Ala Asp Ala Thr Asn Glu His Pro Glu Cys Val Ile Lys
 45 355 . 360 365
 Asp Thr Pro Glu Ala Ala Val Gly Leu Glu Lys Cys Lys Trp Thr Ile
 50 370 . 375 380
 Asn Ala Leu Ile Asn His His Tyr Lys Ile Val Ala Ala Ser Trp Gln
 55 385 . 390 395 400
 Ala Lys Asn Asn Ala Ala Arg Thr Leu Val Met Pro Val Ile Lys Glu
 60 405 . 410 415
 Asn Thr Leu Thr Glu Gly Asn Asn His Trp Asn Leu Val Leu Pro
 65 420 . 425 430
 Ala Trp Gln Tyr Ser Ser Asp Gln Ala Glu Gln Glu Lys Leu Asn Thr
 70 435 . 440 445

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Trp Arg Val Arg Leu Ala Leu Glu Asp Glu Lys Gly Asn Arg Gln Asn
 450 455 460
 5 Ser Gly Val Val Glu Ile Thr Val Gln Gln Asp Arg Lys Ile Glu Leu
 465 470 475 480
 10 Ile Val Asn Asn Ile Ala Asn Pro Glu Glu Asn Asn His Ser His Glu
 485 490 495
 15 Ala Ser Ala Gln Ala Asp Gly Val Asp Gly Val Val Met Asp Leu Asp
 500 505 510
 20 Val Thr Asp Ser Phe Gly Asp Asn Thr Asp Arg Asn Gly Asp Ala Leu
 515 520 525
 25 Pro Glu Asp Asn Leu Thr Pro Gln Leu Tyr Asp Ala Gln Asp Lys Arg
 530 535 540
 30 Val Thr Leu Thr Asn Lys Pro Cys Ser Thr Asp Asn Pro Cys Val Phe
 545 550 555 560
 Ile Ala Lys Gln Asp Lys Glu Lys Gly Thr Val Thr Leu Ser Ser Thr
 565 570 575
 35 Leu Pro Gly Thr Tyr Arg Trp Lys Ala Lys Ala Pro Tyr Asp Asp
 580 585 590
 Ser Asn Tyr Val Asp Val Thr Phe Leu Gly Ala Glu Ile Gly Gly Leu
 595 600 605
 40 Asn Ala Phe Ile Tyr Arg Val Gly Ala Ala Lys Pro Ser Asn Leu Ile
 610 615 620
 45 Gly Lys Asp Lys Glu Pro Leu Pro Ser Thr Thr Phe Ile Asp Leu Phe
 625 630 635 640
 Tyr Gly Ala Thr Thr Ile Lys Thr Val Ser Ser Ser Arg Ser Lys Asn
 645 650 655
 50 Leu Thr Lys Arg Trp Cys Ser Thr Thr Ser Gly Asn Leu Pro Ala
 660 665 670

55

Arg Ala Ser Met Val Ser Gly Cys Thr Gly Glu His Ser Asn Glu Asp
675 680 685

5 Ile Val Ile Pro Ala Thr Asn Arg Glu Ala Ala Gln Thr Tyr Gly Ala
690 695 700

10 Gln Ala Gly Asp Gly Leu Gln Gly Tyr Gly Leu Arg Val Leu Tyr Thr
705 710 715 720

Lys Lys

15

<210> 32
<211> 319.
<212> PRT
20 <213> Escherichia coli
<400> 32

Met Lys Gln Asp Lys Arg Arg Gly Leu Thr Arg Ile Ala Leu Ala Leu
1 5 10 15

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Ala Leu Ala Gly Tyr Cys Val Ala Pro Val Ala Leu Ala Glu Asp Ser
20 25 30

30

Ala Trp Val Asp Ser Gly Glu Thr Asn Ile Phe Gln Gly Thr Ile Pro
35 40 45

35

Trp Leu Tyr Ser Glu Gly Gly Ser Ala Thr Thr Asp Ala Asp Arg Val
50 55 60

40

Thr Leu Thr Ser Asp Leu Lys Gly Ala Arg Pro Gln Gly Met Lys Arg
65 70 75 80

45

Thr Ser Val Phe Thr Arg Val Ile Asn Ile Gly Asp Thr Glu Gly Asp
85 90 95

50

Val Asp Leu Gly Gly Leu Gly Asp Asn Ala Lys Thr Ile Asp Thr Ile
100 105 110

Arg Trp Met Ser Tyr Lys Asp Ala Gln Gly Gly Asp Pro Lys Glu Leu
115 120 125

55

Ala Thr Lys Val Thr Ser Tyr Thr Leu Thr Asp Ala Asp Arg Gly Arg
130 135 140

Tyr Ile Gly Ile Glu Ile Thr Pro Thr Thr Gln Thr Gly Thr Pro Asn
 145 150 155 160

5 Val Gly Thr Ala Leu His Leu Tyr Asp Val Ser Thr Ala Ser Gly Gly
 165 170 175

10 Gly Ser Asp Ser Asp Asn Val Ala Pro Gly Pro Val Val Asn Gln Asn
 180 185 190

15 Leu Lys Val Ala Ile Phe Val Asp Gly Thr Ser Ile Asn Leu Ile Asn
 195 200 205

Gly Ser Thr Pro Ile Glu Leu Gly Lys Thr Tyr Val Ala Lys Leu Tyr
 210 215 220

20 Ser Asp Glu Asn Lys Asn Gly Lys Phe Asp Ala Gly Thr Asp Ala Asp
 225 230 235 240

25 Val Thr Ala Asn Tyr Asp Phe Arg Trp Val Leu Ser Gly Ser Ser Gln
 245 250 255

30 Gln Leu Gly Thr Ser Gly Gly Ile Val Asn Ser Ser Phe Asp Asn Asn
 260 265 270

Asn Leu Val Ile Pro Ala Thr Asn Asp Glu Ala Arg Thr Asn Leu Asn
 275 280 285

35 Gly Pro Ala Arg Asp Gly Lys Glu Ala Leu Ser Ile Pro Thr Asn Gly
 290 295 300

40 Asp Gly Val Gln Gly Tyr Lys Leu His Ile Ile Tyr Lys His Lys
 305 310 315

45 <210> 33

<211> 629

<212> PRT

<213> Escherichia coli

<400> 33

50 Met Lys Lys Val Leu Thr Leu Ser Leu Leu Ala Leu Cys Val Ser His
 1 5 10 15

Ser Ala Val Ala Ala Asn Tyr Thr Phe Asn Asn Asp Asn Ile Ala Leu
 20 25 30

55

5

Ser Phe Asp Asp Thr Asn Ser Thr Ile Val Leu Lys Asp Arg Arg Thr
 35 40 45

Asn His Pro Ile Thr Pro Gln Glu Leu Phe Phe Leu Thr Leu Pro Asp
 50 55 60

10

Glu Thr Lys Ile His Thr Ala Asp Phe Lys Ile Lys His Ile Lys Lys
 65 70 75 80

15

Gln Asp Asn Ala Ile Val Ile Asp Phe Thr Arg Pro Asp Phe Asn Val
 85 90 95

20

Thr Val Gln Leu Asn Leu Val Lys Gly Lys Tyr Ala Ser Ile Asp Tyr
 100 105 110

25

Phe Pro Thr Lys Lys Gln Phe Gln Ala Pro Tyr Val Asp Gly Ala Ile
 130 135 140

30

Thr Ser Ser Pro Ile Ile Ala Asp Ser Phe Phe Ile Leu Pro Asn Lys
 145 150 155 160

35

Pro Ile Val Asn Thr Tyr Ala Tyr Glu Ala Thr Thr Asn Leu Asn Val
 165 170 175

40

Glu Leu Lys Thr Pro Ile Gln Pro Glu Thr Pro Val Ser Phe Thr Thr
 180 185 190

45

Gln Phe Ile Asn Ala Val Arg Pro Arg Pro Tyr Lys Pro Tyr Leu His
 210 215 220

50

Tyr Asn Ser Trp Met Asp Ile Gly Phe Phe Thr Pro Tyr Thr Glu Gln
 225 230 235 240

55

Asp Val Leu Gly Arg Met Asp Glu Trp Asn Lys Glu Phe Ile Ser Gly
 245 250 255

Arg Gly Val Ala Leu Asp Ala Phe Leu Leu Asp Asp Gly Trp Asp Asp
 260 265 270
 5
 Leu Thr Gly Arg Trp Leu Phe Gly Pro Ala Phe Ser Asn Gly Phe Ser
 275 280 285
 10 Lys Val Arg Glu Lys Ala Asp Ser Leu His Ser Ser Val Gly Leu Trp
 290 295 300
 15 Leu Ser Pro Trp Gly Gly Tyr Asn Lys Pro Gln Arg Arg Ser Arg Phe
 305 310 315 320
 Ala Cys Lys Arg Val Trp Val Arg Asn Arg Gly Arg Gln Ala Gly Ala
 325 330 335
 20 Phe Gly Ser Glu Leu Leu Lys Asn Phe Asn Glu Gln Ile Ile Asn Leu
 340 345 350
 25 Ile Lys Asn Glu His Ile Thr Ser Phe Lys Leu Asp Gly Met Gly Asn
 355 360 365
 30 Ala Ser Ser His Ile Lys Gly Ser Pro Phe Ala Ser Asp Phe Asp Ala
 370 375 380
 Ser Ile Ala Leu Leu His Asn Met Arg Arg Ala Asn Pro Asn Leu Phe
 385 390 395 400
 35 Ile Asn Leu Thr Thr Gly Thr Asn Ala Ser Pro Ser Trp Leu Phe Tyr
 405 410 415
 40 Ala Asp Ser Ile Trp Arg Gln Gly Asp Asp Ile Asn Leu Tyr Gly Pro
 420 425 430
 45 Gly Thr Pro Val Gln Gln Trp Ile Thr Tyr Arg Asp Ala Glu Thr Tyr
 435 440 445
 Arg Ser Ile Val Arg Lys Gly Pro Leu Phe Pro Leu Asn Ser Leu Met
 450 455 460
 50 Tyr His Gly Ile Val Ser Ala Glu Asn Ala Tyr Tyr Gly Leu Glu Lys
 465 470 475 480
 55

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Val Gln Thr Asp Ser Asp Phe Ala Asp Gln Val Trp Ser Tyr Phe Ala
 485 490 495

5 Thr Gly Thr Gln Leu Gln Glu Leu Tyr Ile Thr Pro Ser Met Leu Asn
 500 505 510

10 Lys Val Lys Trp Asp Thr Leu Ala Lys Ala Ala Lys Trp Ser Lys Glu
 515 520 525

Asn Ala Ser Val Leu Val Asp Thr His Trp Ile Gly Gly Asp Pro Thr
 530 535 540

15 Ala Leu Ala Val Tyr Gly Trp Ala Ser Trp Ser Lys Asp Lys Ala Ile
 545 550 555 560

20 Leu Gly Leu Arg Asn Pro Ser Asp Lys Pro Gln Thr Tyr Tyr Leu Asp
 565 570 575

25 Leu Ala Lys Asp Phe Glu Ile Pro Ala Gly Asn Ala Ala Gln Phe Ser
 580 585 590

Leu Lys Ala Val Tyr Gly Ser Asn Lys Thr Val Pro Val Glu Tyr Lys
 595 600 605

30 Asn Ala Thr Val Ile Thr Leu Gln Pro Leu Glu Thr Leu Val Phe Glu
 610 615 620

35 Ala Val Thr Ile Asn
 625

40 <210> 34
 <211> 1778
 <212> PRT
 <213> Escherichia coli
 <400> 34

45 Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr
 1 5 10 15

50 Thr Val Ala Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
 20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Leu Leu Ser Ser
 35 40 45

55

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Phe Gly Ala Ser Ala Asp Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly
50 55 60

Asp Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly Ala Lys
65 70 75 80

Ala Asn Thr Phe Met Asn Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr
10 85 90 95

Asp Ala Ile Ala Glu Gly Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr
15 100 105 110

Leu Ala Thr Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala Lys Ala
115 120 125

Met Gly Asp Arg Ser Val Ala Leu Gly Ala Ser Ser Val Ala Asn Gly
20 130 135 140

Asp Arg Ser Met Ala Phe Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr
25 145 150 155 160

Ser Leu Ala Ile Gly Asp Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile
30 165 170 175

Ala Leu Gly Asn Thr Ala Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu
180 185 190

Gly Asp Asn Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala
35 195 200 205

Ser Ser Lys Ala Gly Gly Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser
40 210 215 220

Thr Ala Asn Ser Thr Gly Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser
45 225 230 235 240

Ser Asn Asp Asn Ala Ile Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly
245 250 255

Val Asn Ser Met Ala Leu Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser
50 260 265 270

5 Ser Ile Ala Leu Gly Asn Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile
275 280 285

10 Ala Leu Gly Gln Gly Ser Ile Ala Ser Lys Val Asn Ser Ile Ala Leu
290 295 300

15 Gly Ser Asn Ser Leu Ser Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu
305 310 315 320

Gly Ser Ala Ala Gly Gly Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser
325 330 335

20 Arg Ala Asn Gly Asn Asp Ser Val Ala Ile Gly Val Gly Ala Ala Ala
340 345 350

25 Ala Thr Asp Asn Ser Val Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala
355 360 365

30 Ser Asn Thr Val Ser Val Gly Asn Ser Ala Thr Lys Arg Lys Ile Val
370 375 380

Asn Met Ala Ala Gly Ala Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn
385 390 395 400

35 Gly Ser Gln Leu Tyr Thr Ile Ser Asp Ser Val Ala Lys Arg Leu Gly
405 410 415

40 Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala Val Ser Tyr
420 425 430

45 Ala Leu Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly
435 440 445

Ile Asp Asn Asn Thr Leu Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser
450 455 460

50 Ala Asn His Gly Ala Asn Ala Thr Asn Lys Ile Thr Asn Val Ala Lys
465 470 475 480

55 Gly Thr Val Ser Ala Thr Ser Thr Asp Val Val Asn Gly Ser Gln Leu
485 490 495

Tyr Asp Leu Gln Gln Asp Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser

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	500	505	510
5	Ala Ala His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala 515	520	525
10	Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu 530	535	540
15	Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Asn Ile Ala Thr 545	550	555
20	Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly 565	570	575
25	Asp Asp Ser Leu Leu Trp Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala 580	585	590
30	His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn 595	600	605
35	Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr 610	615	620
40	Thr Asn Asp Asn Val Thr Thr Asn Thr Asn Ile Ala Thr Asn Thr 625	630	635
45	Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp 645	650	655
50	Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly 660	665	670
55	Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr 675	680	685
	Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn 690	695	700
	Asp Asn Val Thr Thr Asn Thr Asn Ile Ala Thr Asn Thr Thr Asn 705	710	715
	Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu 725	730	735

Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp
 740 745 750

5

Ala Thr Ser Lys Ile Thr Asn Val Lys Ala Gly Asp Leu Thr Ala Gly
 755 760 765

10

Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn
 770 775 780

15

Val Ser Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn
 785 790 795 800

20

Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe
 805 810 815

25

Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys
 820 825 830

30

Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Ile Thr
 850 855 860

35

Asn Leu Thr Asp Ser Val Gly Asp Leu Lys Asp Asp Ser Leu Leu Trp
 865 870 875 880

35

Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr
 885 890 895

40

Ser Lys Ile Thr Asn Leu Leu Ala Gly Lys Ile Ser Ser Asn Ser Thr
 900 905 910

45

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val Ala Asp Ser Phe Thr
 915 920 925

50

Ser Tyr Leu Gly Gly Ala Asp Ile Ser Asp Thr Gly Val Leu Ser
 930 935 940

55

Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp
 945 950 955 960

Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr Ser Leu Gly Asp Ala
 965 970 975
 5
 Leu Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Ile
 980 985 990
 10
 Asn Asn Ala Pro Ser Val Ile Thr Asp Val Ala Asn Gly Ala Val Ser
 995 1000 1005
 15
 Ser Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val
 1010 1015 1020
 Ser Asp Tyr Ile Ala Asp Ala Leu Gly Gly Asn Ala Val Val Asn
 1025 1030 1035
 20
 Thr Asp Gly Ser Ile Thr Thr Pro Thr Tyr Ala Ile Ala Gly Gly
 1040 1045 1050
 25
 Ser Tyr Asn Asn Val Gly Asp Ala Leu Glu Ala Ile Asp Thr Thr
 1055 1060 1065
 Leu Asp Asp Ala Leu Leu Trp Asp Thr Thr Ala Asn Gly Gly Asn
 1070 1075 1080
 30
 Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val
 1085 1090 1095
 35
 Ile Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp
 1100 1105 1110
 40
 Ala Ile Asn Gly Ser Gln Leu Tyr Ser Thr Asn Lys Tyr Ile Ala
 1115 1120 1125
 45
 Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile
 1130 1135 1140
 Thr Ala Pro Thr Tyr Thr Ile Ala Asn Thr Asp Tyr Asn Asn Val
 1145 1150 1155
 50
 Gly Glu Ala Leu Asp Ala Leu Asp Asn Asn Ala Leu Leu Trp Asp
 1160 1165 1170
 55

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Glu Asp Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Asn Ala Ser
 1175 1180 1185

 5 Lys Ile Thr Asn Val Ala Ala Gly Asp Leu Ser Thr Thr Ser Thr
 1190 1195 1200

 10 Asp Ala Val Asn Gly Ser Gln Leu Asn Ala Thr Asn Ile Leu Val
 1205 1210 1215

 15 Thr Gln Asn Ser Gln Met Ile Asn Gln Leu Ala Gly Asn Thr Ser
 1220 1225 1230

 20 Glu Thr Tyr Ile Glu Glu Asn Gly Ala Gly Ile Asn Tyr Val Arg
 1235 1240 1245

 25 Thr Asn Asp Ser Gly Leu Ala Phe Asn Asp Ala Ser Ala Ser Gly
 1250 1255 1260

 Ile Gly Ala Thr Ala Val Gly Tyr Asn Ala Val Ala Ser His Ala
 265 1270 1275

 30 Ser Ser Val Ala Ile Gly Gln Asp Ser Ile Ser Glu Val Asp Thr
 1280 1285 1290

 Gly Ile Ala Leu Gly Ser Ser Ser Val Ser Ser Arg Val Ile Val
 1295 1300 1305

 35 Lys Gly Thr Arg Asn Thr Ser Val Ser Glu Glu Gly Val Val Ile
 1310 1315 1320

 40 Gly Tyr Asp Thr Thr Asp Gly Glu Leu Leu Gly Ala Leu Ser Ile
 1325 1330 1335

 Gly Asp Asp Gly Lys Tyr Arg Gln Ile Ile Asn Val Ala Asp Gly
 1340 1345 1350

 45 Ser Glu Ala His Asp Ala Val Thr Val Arg Gln Leu Gln Asn Ala
 1355 1360 1365

 50 Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr Tyr His Ala Asn
 1370 1375 1380

 Ser Thr Ala Glu Asp Ser Leu Ala Val Gly Glu Asp Ser Leu Ala

55

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	1385	1390	1395
5	Met Gly Ala Lys Thr Ile Val Asn Gly Asn Ala Gly		Ile Gly Ile
	1400	1405	1410
10	Gly Leu Asn Thr Leu Val Leu Ala Asp Ala Ile Asn		Gly Ile Ala
	1415	1420	1425
	Ile Gly Ser Asn Ala Arg Ala Asn His Ala Asp Ser		Ile Ala Met
	1430	1435	1440
15	Gly Asn Gly Ser Gln Thr Thr Arg Gly Ala Gln Thr		Asn Tyr Thr
	1445	1450	1455
20	Ala Tyr Asn Met Asp Ala Pro Gln Asn Ser Val Gly		Glu Phe Ser
	1460	1465	1470
	Val Gly Ser Glu Asp Gly Gln Arg Gln Ile Thr Asn		Val Ala Ala
	1475	1480	1485
25	Gly Ser Ala Asp Thr Asp Ala Val Asn Val Gly Gln		Leu Lys Val
	1490	1495	1500
30	Thr Asp Ala Gln Val Ser Gln Asn Thr Gln Ser Ile		Thr Asn Leu
	1505	1510	1515
35	Asn Thr Gln Val Thr Asn Leu Asp Thr Arg Val Thr		Asn Ile Glu
	1520	1525	1530
	Asn Gly Ile Gly Asp Ile Val Thr Thr Gly Ser Thr		Lys Tyr Phe
	1535	1540	1545
40	Lys Thr Asn Thr Asp Gly Ala Asp Ala Asn Ala Gln		Gly Lys Asp
	1550	1555	1560
45	Ser Val Ala Ile Gly Ser Gly Ser Ile Ala Ala Ala		Asp Asn Ser
	1565	1570	1575
50	Val Ala Leu Gly Thr Gly Ser Val Ala Asp Glu Glu		Asn Thr Ile
	1580	1585	1590
55	Ser Val Gly Ser Ser Thr Asn Gln Arg Arg Ile Thr		Asn Val Ala
	1595	1600	1605

5

Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser Gln Leu Lys
 1610 1615 1620

10

Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp Thr Lys Ala Asp Gly
 1625 1630 1635

15

Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly Asn Ser Gly
 1640 1645 1650

20

Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn Asp
 1655 1660 1665

25

Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys
 1670 1675 1680

Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser
 1685 1690 1695

30

Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala
 1700 1705 1710

35

Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala
 1715 1720 1725

Ser Ile Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu
 1730 1735 1740

40

Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu
 1745 1750 1755

45

Gln Gly Ser Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly
 1760 1765 1770

Ala Gly Ile Gln Trp
 1775

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<210> 35
 <211> 227
 <212> PRT
 <213> Escherichia coli
 <400> 35

Met Asn Leu Lys Lys Thr Leu Leu Ser Val Leu Met Ile Leu Gln Leu

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5	Cys Leu Leu Val Gly Cys Asp Tyr Ile Glu Lys Ala Ser Lys Val Asp 20	25	30
10	Asp Leu Val Thr Gln Gln Glu Leu Gln Lys Ser Lys Ile Glu Ala Leu 35	40	45
15	Glu Lys Gln Gln Glu Leu Asp Lys Arg Lys Ile Glu His Phe Glu Lys 50	55	60
20	Gln Gln Thr Thr Ile Ile Asn Ser Thr Lys Thr Leu Ala Gly Val Val 65	70	75
			80
25	Lys Ala Val Lys Asn Lys Gln Asp Glu Phe Val Phe Thr Glu Phe Asn 85	90	95
30	Pro Ala Gln Thr Gln Tyr Phe Ile Leu Asn Asn Gly Ser Val Gly Leu 100	105	110
35	Ala Gly Lys Ile Leu Ser Ile Asp Ala Val Glu Asn Gly Ser Val Ile 115	120	125
40	Arg Ile Ser Leu Val Asn Leu Leu Ser Val Pro Val Ser Asn Met Gly 130	135	140
45	Phe Tyr Ala Thr Trp Gly Gly Glu Lys Pro Thr Asp Ile Asn Ala Leu 145	150	155
			160
50	Ala Lys Trp Gln Gln Leu Leu Phe Ser Thr Ala Met Asn Ser Ser Leu 165	170	175
55	Lys Leu Leu Pro Gly Gln Trp Gln Asp Ile Asn Leu Thr Leu Lys Gly 180	185	190
60	Val Ser Pro Asn Asn Leu Lys Tyr Leu Lys Leu Ala Ile Asn Met Ala 195	200	205
65	Asn Ile Gln Phe Asp Arg Leu Gln Pro Ala Glu Ser Pro Gln Arg Lys 210	215	220
70	Asn Lys Lys 225		

5 <210> 36
 <211> 1109
 <212> PRT
 <213> Escherichia coli
 <400> 36

10 Met Lys Arg Val Val Arg Leu Leu Gly Val Gly Leu Leu Leu Val
 1 5 10 15

15 Val Leu Leu Leu Ile Leu Phe Val Leu Ala Gln Thr Thr Pro Leu Ile
 20 25 30

20 Ser Ala Gln Asp Glu His Ala Val Trp Leu Arg Leu Leu Ile Thr Ala
 35 40 45

25 Ile Val Ile Cys Leu Leu Ser Met Cys Ile Phe Phe Leu Phe Ser Phe
 50 55 60

30 Arg Gln Asn Glu Ala Ser Thr Ile Ser Leu Tyr Ala Gln Pro Thr Asp
 65 70 80

35 Ile Lys Glu Ile Asn Thr Glu Gln Pro Asn Tyr Ala Ser Leu Thr
 85 90 95

40 Ile Tyr Leu Arg Asp Arg Tyr Gly Pro Phe Trp Arg Arg Lys Val Arg
 100 105 110

45 Leu Leu Leu Val Thr Gly Glu Pro Glu Gln Ala Glu Ala Ile Ala Pro
 115 120 125

50 Gly Leu Thr Gly Gln His Trp Leu Glu Gly Asp His Thr Val Leu Ile
 130 135 140

55 Tyr Gly Gly Arg Pro Thr Ala Glu Pro Asp Val Thr Leu Leu Thr Ala
 145 150 155 160

60 Leu Lys Lys Leu Arg Arg Ser Arg Pro Leu Asp Gly Ile Ile Trp Ala
 165 170 175

65 Leu Thr Glu Glu Gln Ser Arg Gln Thr Ala Gln Leu Asp Lys Gly Trp
 180 185 190

70 Arg Gly Leu Ile Asn Gly Gly Lys Arg Leu Gly Phe Gln Ala Pro Leu

75

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	195	200	205
5	Tyr Leu Trp Gln Val Cys Asp Asp Gly Asp Tyr Gln Thr Gly Arg Pro 210	215	220
10	Leu Gln Ser Val Gly Cys Leu Leu Pro Glu Arg Cys Thr Pro Glu Gln 225	230	235
15	Leu Ala Val Met Leu Glu Ala Ala Ala Asp Gly Thr Gly His Val Ala 245	250	255
20	Ala Thr Asp Arg Tyr Arg Met Phe Ser Ala Ala Ser Gly Ser Tyr Pro 260	265	270
25	Cys Arg Ala Gly Tyr Cys Ser Leu Ala Asp Arg Pro Glu Thr Ala Ala 275	280	285
30	Gly Arg Arg Arg Ile Phe Phe Pro Ala Pro Ala Arg Pro Asp Val Gln 290	295	300
35	Pro Ala Ala Cys Arg Arg Ala Gly Gly Gln His Leu Met Gln Trp Leu 305	310	315
40	Pro Ser Pro Val Trp Ala Gly Val Thr Val Ile Thr Arg Ala Gly Ala 325	330	335
45	Arg Trp Val Phe Leu Trp Leu Arg Thr Ala Leu Met Ser Ala Val Cys 340	345	350
50	Val Leu Val Ile Trp Gly Ala Gly Met Thr Thr Ser Phe Phe Ala Asn 355	360	365

Phe Pro Gly Tyr Ala Gln Ala Ala Asn Arg Leu Val Arg Asp Val Ala
435 440 445

5
Val Asp His Leu Gln Gln Leu Asn Ala Phe Val Ala Leu Pro Pro
450 455 460

10 Asn Ser Pro Gln Arg Thr Ala Thr Gly Glu Gln Arg Tyr Lys Gln Leu
465 470 475 480

15 Lys Ala Leu Leu Met Thr Ser Arg Pro Glu Lys Ala Asp Ala Ala Phe
485 490 495

20 Phe Ser Thr Thr Leu Met Ala Asp Gly Leu Arg Tyr Glu Asn Ile Pro
500 505 510

25 Glu Gly Val Arg Gln Ser Val Leu Pro Ser Leu Leu Thr Phe Trp Thr
515 520 525

30 Ala Asn Leu Pro Glu His Pro Gln Trp Lys Thr Ser Pro Pro Pro Glu
530 535 540

35 Leu Thr Gly Ala Val Arg Lys Ile Leu Leu Arg Gln Ile Gly Val Arg
545 550 555 560

40 Asn Ala Glu Asn Thr Leu Tyr Gln Asn Val Leu Gln Gln Val Ser Arg
565 570 575

45 Asn Tyr Ala Asp Met Thr Leu Ala Asp Met Thr Gly Asp Thr Leu Thr
580 585 590

50 Glu Ser Leu Phe Ser Thr Glu Gln Thr Val Pro Gly Met Phe Thr Arg
595 600 605

55 Gln Ala Trp Glu Gly Gln Val Arg Glu Ala Ile Glu Gln Val Val Thr
610 615 620

60 Ala Arg Arg Glu Glu Ile Asp Trp Val Leu Ser Asp Arg Gln Gln Asp
625 630 635 640

65 Thr Ser Ala Asp Ile Ser Pro Asp Thr Leu Arg Asn Arg Leu Thr Ser
645 650 655

Arg Tyr Phe Thr Asp Phe Ala Gly Ser Trp Leu Ala Phe Leu Asn Ser
 660 665 670

5 Ile His Trp Lys Lys Glu Asp Ser Leu Ser Gly Ile Leu Asp Gln Leu
 675 680 685

10 Thr Leu Met Ala Asp Ala Arg Gln Ser Pro Leu Ile Ala Leu Thr Asp
 690 695 700

15 Thr Leu Ala Trp Gln Ala Ala Thr Gly Arg Glu Asn Arg Gly Leu Ser
 705 710 715 720

Asp Ser Leu Ala Lys Ser Ala Gln Glu Leu Phe Asn Gly Lys Glu Lys
 725 730 735

20 Thr Pro Gln Gln Ser Arg Glu Gly Asp Asp Val Pro Val Gly Pro Leu
 740 745 750

25 Asp Lys Thr Phe Thr Pro Leu Leu Arg Leu Leu Gly Asp Lys Ala Gly
 755 760 765

30 Gly Gly Asp Ser Gln Leu Ser Leu Gln Thr Tyr Leu Thr Arg Val Thr
 770 775 780

Arg Val Arg Leu Lys Leu Gln Gln Val Thr Asn Ala Pro Asp Pro Gln
 785 790 795 800

35 Glu Met Thr Gln Gln Leu Ala Gln Thr Val Leu Gln Gly Lys Thr Val
 805 810 815

40 Asp Leu Thr Asp Thr Arg Asp Tyr Gly Arg Leu Ile Ala Ala Ser Leu
 820 825 830

45 Gly Glu Glu Trp Ser Gly Phe Gly Gln Ala Leu Phe Val Arg Pro Val
 835 840 845

Glu Gln Ser Trp Arg Gln Val Leu Thr Pro Ala Ala Asp Ser Leu Asn
 850 855 860

50 Arg Gln Trp Gln Arg Ala Ile Val Ser His Trp Asn Gln Asp Phe Ala
 865 870 875 880

55

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Gly Arg Tyr Pro Phe Lys Ala Ser Gln Asn Asp Ala Ser Leu Pro Leu
 885 890 895

5 Leu Ala Gln Tyr Leu Arg Asp Asp Gly Arg Ile Asn Leu Phe Ile Ala
 900 905 910

10 Ala Asn Leu Ser Gly Val Leu Lys Arg Glu Gly Arg Tyr Trp Val Ala
 915 920 925

Asp Ala Met Asn Thr Gln Gly Leu Thr Val Asn Pro Asp Phe Ile Arg
 930 935 940

15 Ala Leu Asn Arg Leu Arg Asp Val Ala Asp Thr Ala Phe Ala Ser Gly
 945 950 955 960

20 Asp Ala Gly Ile His Phe Glu Leu Arg Ala Lys Pro Ala Arg Asp Val
 965 970 975

25 Met Lys Thr His Leu Val Ile Asp Gly Gln Glu Leu Glu Tyr Phe Asn
 980 985 990

Gln Lys Glu Arg Trp Gln Arg Phe Asn Trp Pro Asp Glu Gln Trp Gln
 995 1000 1005

30 Pro Gly Ala Ser Leu Ser Trp Thr Ser Thr Gln Ala Met Glu Arg
 1010 1015 1020

35 Ile Leu Ala Asp Tyr Arg Gly Ser Trp Ser Leu Ile Arg Leu Leu
 1025 1030 1035

40 Glu Gln Ala Gln Val Thr Pro Val Asp Ser Ser Thr Phe Lys Val
 1040 1045 1050

Val Trp Lys Ala Gln Asp Gly Leu Pro Leu Asn Tyr Leu Leu Arg
 1055 1060 1065

45 Val Glu Gln Gly Lys Gly Pro Leu Ala Leu Leu Glu Leu Lys Asn
 1070 1075 1080

50 Phe Arg Leu Pro Gly Gln Val Phe Leu Thr Gly Lys Ser Met Lys
 1085 1090 1095

55 Asp Val Glu Glu Tyr Gly Glu Asp Ala Asp Glu

	1100	1105	
5	<210> 37 <211> 178 <212> PRT <213> Escherichia coli <400> 37		
10	Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met		
	1 5 10 15		
15	Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp		
	20 25 30		
	Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile		
	35 40 45		
20	Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu		
	50 55 60		
25	Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg		
	65 70 75 80		
30	Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu		
	85 90 95		
	Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys		
	100 105 110		
35	Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln		
	115 120 125		
40	Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp		
	130 135 140		
45	Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro		
	145 150 155 160		
	Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys		
	165 170 175		
50	Asp Lys		

55

<210> 38
 <211> 280
 <212> PRT
 5 <213> Escherichia coli
 <400> 38

Met Ile Ser Gly Gly Asn Met Leu Lys Glu Trp Met Ile Phe Thr Cys
 1 5 10 15

10 Ser Leu Leu Thr Leu Ala Gly Ala Ser Leu Pro Leu Ser Gly Cys Ile
 20 25 30

15 Ser Arg Gly Gln Glu Ser Ile Ser Glu Gly Ala Ala Phe Gly Ala Gly
 35 40 45

20 Ile Leu Arg Glu Pro Gly Ala Thr Lys Lys Ala Asp Thr Lys Asp Leu
 50 55 60

25 Asn Val Pro Pro Pro Val Tyr Gly Pro Pro Gln Val Ile Phe Arg Ile
 65 70 75 80

30 Asp Asp Asn Arg Tyr Phe Thr Leu Glu Asn Tyr Thr His Cys Glu Asn
 85 90 95

35 Gly Gln Thr Phe Tyr Asn Asn Lys Ala Lys Asn Ile His Val Lys Ile
 100 105 110

40 Leu Asp Ala Ser Gly Tyr Leu Phe Lys Gly Arg Leu Phe Trp Leu Ser
 115 120 125

45 Thr Arg Asp Asp Phe Leu Ala Phe Pro Ala Thr Leu Asn Thr Arg His
 130 135 140

50 Ala Ser Cys Met Gly Ser Asn Lys Gly Cys Met Asn Ala Val Ile Val
 145 150 155 160

55 Thr Thr Asp Gly Gly Lys Arg Arg Ser Gly Val Pro Tyr Gly Ser Tyr
 165 170 175

60 Thr Gln Asn Pro Thr Gly Ala Thr Arg Asp Tyr Asp Met Leu Val Met
 180 185 190

65 Asn Asp Gly Phe Tyr Leu Leu Arg Tyr Arg Gly Gly Gln Gly Arg Phe
 195 200 205

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Ser Pro Val Ile Leu Arg Trp Ile Leu Ser Thr Glu Asp Ser Ser Gly
210 215 220

5 Val Val Arg Ser Glu Asp Ala Tyr Glu Leu Phe Arg Pro Gly Glu Glu
225 230 235 240

10 Val Pro Ser Thr Gly Phe Tyr Lys Ile Asp Leu Ser Arg Phe Tyr Pro
245 250 255

15 Lys Asn Asn Val Met Glu Met Gln Cys Asp Arg Thr Leu Glu Pro Val
260 265 270

Gln Pro Ser Glu Ser Lys Ile Gln
275 280

20 <210> 39
<211> 501
<212> PRT
<213> Escherichia coli
25 <400> 39
Met Glu His Val Ser Ile Lys Thr Leu Tyr His Leu Leu Cys Cys Met
1 5 10 15

30 Leu Leu Phe Ile Ser Ala Met Cys Ala Leu Ala Gln Glu His Glu Pro
20 25 30

35 Ile Gly Ala Gln Asp Glu Arg Leu Ser Thr Leu Ile His Gln Arg Met
35 40 45

40 Gln Glu Ala Lys Val Pro Ala Leu Ser Val Ser Val Thr Ile Lys Gly
50 55 60

45 Val Arg Gln Arg Phe Val Tyr Gly Val Ala Asp Val Ala Ser Gln Lys
65 70 75 80

50 Ala Asn Thr Leu Asp Thr Val Tyr Glu Leu Gly Ser Met Ser Lys Ala
85 90 95

55 Phe Thr Gly Leu Val Val Gln Ile Leu Ile Gln Glu Gly Arg Leu Arg
100 105 110

Gln Gly Asp Asp Ile Ile Thr Tyr Leu Pro Glu Met Arg Leu Asn Tyr
115 120 125

55

5

Gln Gly Lys Pro Ala Ser Leu Thr Val Ala Asp Phe Leu Tyr His Thr
 130 135 140

Ser Gly Leu Pro Phe Ser Thr Leu Ala Arg Leu Glu Asn Pro Met Pro
 145 150 155 160

10

Gly Ser Ala Val Ala Gln Gln Leu Arg Asn Glu Asn Leu Leu Phe Ala
 165 170 175

15

Pro Gly Ala Lys Phe Ser Tyr Ala Ser Ala Asn Tyr Asp Val Leu Gly
 180 185 190

20

Ala Val Ile Glu Asn Val Thr Gly Lys Thr Phe Thr Glu Val Ile Ala
 195 200 205

25

Glu Arg Leu Thr Gln Pro Leu Gly Met Ser Ala Thr Val Ala Val Lys
 210 215 220

Gly Asp Glu Ile Ile Val Asn Lys Ala Ser Gly Tyr Lys Leu Gly Phe
 225 230 235 240

30

Gly Lys Pro Val Leu Phe His Ala Pro Leu Ala Arg Asn His Val Pro
 245 250 255

35

Ala Ala Tyr Ile His Ser Thr Leu Pro Asp Met Glu Ile Trp Ile Asp
 260 265 270

40

Ala Trp Leu His Arg Lys Ala Leu Pro Ala Thr Leu Arg Glu Ala Met
 275 280 285

Ser Asn Ser Trp Arg Gly Asn Ser Asp Val Pro Leu Ala Ala Asp Asn
 290 295 300

45

Arg Ile Leu Tyr Ala Ser Gly Trp Phe Ile Asp Gln Asn Gln Gly Pro
 305 310 315 320

50

Tyr Ile Ser His Gly Gly Gln Asn Pro Asn Phe Ser Ser Cys Ile Ala
 325 330 335

55

Leu Arg Pro Asp Gln Gln Ile Gly Ile Val Ala Leu Ala Asn Met Asn
 340 345 350

Ser Asn Leu Ile Leu Gln Leu Cys Ala Asp Ile Asp Asn Tyr Leu Arg
 355 360 365

5 Ile Gly Lys Tyr Ala Asp Gly Ala Gly Asp Ala Ile Thr Ala Thr Asp
 370 375 380

10 Thr Leu Phe Val Tyr Leu Thr Leu Leu Leu Cys Phe Trp Gly Ala Val
 385 390 395 400

15 Val Val Val Arg Gly Ala Phe Arg Val Tyr Arg Ala Thr Ala His Gly
 405 410 415

20 Pro Gly Lys Gln Gln Arg Leu Arg Leu Arg Val Arg Asp Tyr Ile Ile
 420 425 430

25 Ala Leu Ala Val Pro Gly Leu Val Ala Ala Met Leu Tyr Val Ala Pro
 435 440 445

30 Gly Ile Leu Ser Pro Gly Leu Asp Trp Arg Phe Ile Leu Val Trp Gly
 450 455 460

35 Pro Ser Ser Val Leu Ala Ile Pro Phe Gly Ile Ile Leu Leu Ala Phe
 465 470 475 480

40 Val Leu Thr Leu Asn His Gln Ile Lys Arg Ile Leu Leu His Asn Lys
 485 490 495

45 Glu Trp Asp Asp Glu
 500

50 <210> 40
 <211> 682
 <212> PRT
 <213> Escherichia coli
 <400> 40

55 Met Lys Asn Lys Tyr Ile Ile Ala Pro Gly Ile Ala Val Met Cys Ser
 1 5 10 15

Ala Val Ile Ser Ser Gly Tyr Ala Ser Ser Asp Lys Lys Glu Asp Thr
 20 25 30

Leu Val Val Thr Ala Ser Gly Phe Thr Gln Gln Leu Arg Asn Ala Pro
 35 40 45

5

Ala Ser Val Ser Val Ile Thr Ser Glu Gln Leu Gln Lys Lys Pro Val
 50 55 60

10

Ser Asp Leu Val Asp Ala Val Lys Asp Val Glu Gly Ile Ser Ile Thr
 65 70 75 80

15

Gly Gly Asn Glu Lys Pro Asp Ile Ser Ile Arg Gly Leu Ser Gly Asp
 85 90 95

20

Tyr Thr Leu Ile Leu Val Asp Gly Arg Arg Gln Ser Gly Arg Glu Ser
 100 105 110

25

Arg Pro Asn Gly Ser Gly Gly Phe Glu Ala Gly Phe Ile Pro Pro Val
 115 120 125

30

Glu Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met Ser Ser Leu
 130 135 140

35

Tyr Gly Ser Asp Ala Ile Gly Gly Val Ile Asn Ile Ile Thr Lys Pro
 145 150 155 160

40

Val Asn Asn Gln Thr Trp Asp Gly Val Leu Gly Leu Gly Gly Ile Ile
 165 170 175

45

Gln Glu His Gly Lys Phe Gly Asn Ser Thr Thr Asn Asp Phe Tyr Leu
 180 185 190

50

Ser Gly Pro Leu Ile Lys Asp Lys Leu Gly Leu Gln Leu Tyr Gly Gly
 195 200 205

55

Met Asn Tyr Arg Lys Glu Asp Ser Ile Ser Gln Gly Thr Pro Ala Lys
 210 215 220

60

Asp Asn Lys Asn Ile Thr Ala Thr Leu Gln Phe Thr Pro Thr Glu Ser
 225 230 235 240

65

Gln Lys Phe Val Phe Glu Tyr Gly Lys Asn Asn Gln Val His Thr Leu
 245 250 255

70

Thr Pro Gly Glu Ser Leu Asp Ala Trp Thr Met Arg Gly Asn Leu Lys
 260 265 270

75

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Gln Pro Asn Ser Lys Arg Glu Thr His Asn Ser Arg Ser His Trp Val
275 280 285

5 Ala Ala Trp Asn Ala Gln Gly Glu Ile Leu His Pro Glu Ile Ala Val
290 295 300

10 Tyr Gln Glu Lys Val Ile Arg Glu Val Lys Ser Gly Lys Lys Asp Lys
305 310 315 320

Tyr Asn His Trp Asp Leu Asn Tyr Glu Ser Arg Lys Pro Glu Ile Thr
 325 330 335

Asn Thr Ile Ile Asp Ala Lys Val Thr Ala Phe Leu Pro Glu Asn Val
340 345 350

20 Leu Thr Ile Gly Gly Gln Phe Gln His Ala Glu Leu Arg Asp Asp Ser

25 Ala Thr Gly Lys Lys Thr Thr Glu Thr Gln Ser Val Ser Ile Lys Gln

Lys Ala Val Phe Ile Glu Asn Glu Tyr Ala Ala Thr Asp Ser Leu Ala

Leu Thr Gly Gly Leu Arg Leu Asp Asn His Glu Ile Tyr Gly Ser Tyr

35 Trp Asn Pro Arg Leu Tyr Ala Val Tyr Asn Leu Thr Asp Asn Leu Thr
122 123 124 125 126 127 128

40 Leu Lys Gly Gly Ile Ala Lys Ala Phe Arg Ala Pro Ser Ile Arg Glu
405 410 415

Val Ser Pro Gly Phe Gly Thr Leu Thr Gln Gly Gly Ala Ser Ile Met
150 155 160

Tyr Gly Asn Arg Asp Leu Lys Pro Glu Thr Ser Val Thr Glu Glu Ile
 465 470 475 480

50 Gly Ile Ile Tyr Ser Asn Asp Ser Gly Phe Ser Ala Ser Ala Thr Leu

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Phe Asn Thr Asp Phe Lys Asn Lys Leu Thr Ser Tyr Asp Ile Gly Thr
 500 505 510

5 Lys Asp Pro Val Thr Gly Leu Asn Thr Phe Ile Tyr Asp Asn Val Gly
 515 520 525

10 Glu Ala Asn Ile Arg Gly Val Glu Leu Ala Thr Gln Ile Pro Val Tyr
 530 535 540

Asp Lys Trp His Val Ser Ala Asn Tyr Thr Phe Thr Asp Ser Arg Arg
 545 550 555 560

15 Lys Ser Asp Asp Glu Ser Leu Asn Gly Lys Ser Leu Lys Gly Glu Pro
 565 570 575

20 Leu Glu Arg Thr Pro Arg His Ala Ala Asn Ala Lys Leu Glu Trp Asp
 580 585 590

25 Tyr Thr Gln Asp Ile Thr Phe Tyr Ser Ser Leu Asn Tyr Thr Gly Lys
 595 600 605

Gln Ile Trp Ala Ala Gln Arg Asn Gly Ala Lys Val Pro Arg Val Arg
 610 615 620

30 Asn Gly Phe Thr Ser Met Asp Ile Gly Leu Asn Tyr Gln Ile Leu Pro
 625 630 635 640

35 Asp Thr Leu Ile Asn Phe Ala Val Leu Asn Val Thr Asp Arg Lys Ser
 645 650 655

40 Glu Asp Ile Asp Thr Ile Asp Gly Asn Trp Gln Val Asp Glu Gly Arg
 660 665 670

Arg Tyr Trp Ala Asn Val Arg Val Ser Phe
 675 680

45 <210> 41
 <211> 164
 <212> PRT
 <213> Escherichia coli
 50 <400> 41

Met Gly Phe Arg Lys Thr Ile Ile Thr Ser Val Gly Leu Ile Phe Ile
 1 5 10 15

55

Ser Phe Ser Phe Val Ala Lys Cys Ser Gln Leu Lys Asn Leu Asn Asn
 2C 25 30

5 Tyr Ser Val Met Leu Cys Gly Lys Val Ser Asn Asn Ile Leu Asp Asp
 35 40 45

10 Ile Gly Gly Tyr Lys Glu Arg Asn Ile Leu Met Leu Arg Ala Ile Lys
 50 55 60

15 Lys Ile Ile Ile Met Thr Ile Val Asn Ile Ile Phe Phe Tyr Ser Phe
 65 70 75 80

Gln Ser Thr Ala Asp Glu Met Val Leu Ile Lys Lys Tyr Gly Phe Gly
 85 90 95

20 Leu Glu Arg Asp Ile Lys Gly Arg Pro Leu Ile Tyr Pro Ile Glu Asn
 100 105 110

25 Tyr Asp Glu Cys Lys Lys Cys Asn His Met Asn Tyr Ile Ala Asp
 115 120 125

30 Val Asn Ala Gln Leu Ala Met Ser Lys Lys Asn Asn Arg Ile Phe Ala
 130 135 140

Asn Ile Thr Phe Thr Asn Asn Ser Ser Thr Thr Tyr Phe Phe Leu Asn
 145 150 155 160

35 Ile Ile Tyr Leu

40 <210> 42
 <211> 218
 <212> PRT
 <213> Escherichia coli
 <400> 42

45 Met Asn Gln Ile Lys Asp Asn Lys Val Ile Met Lys Ile Lys Asn Leu
 1 5 10 15

50 Ile Ser Val Ile Leu Leu Ser Gly Gly Ile Met Gly Thr Gly Leu Tyr
 20 25 30

Ser Ser Asp Asn His Gln Lys Ile Arg Ser Arg Phe Asn Ile Gln Glu
 35 40 45

55

5

Ser Tyr Cys Ala Ile Lys Thr Asn Gly Val Leu Gly Phe Ser Asn Arg
 50 55 60

65

Lys Asp Val Leu Arg Glu Asn Gly Asp Ser Thr Gly Thr Thr Ser Ser
 65 70 75 80

10

Ser Thr Asn Ala Met Met Leu Met Glu Asn Gly Glu Asn Glu Ile Ser
 85 90 95

15

Leu Glu Ile Gly Ala Leu Arg Trp Phe Ser Asp Lys Pro Ala Ser Thr
 100 105 110

20

Glu Glu Arg Gly His Phe Ser Gln Lys Ala Gly Cys Ser Leu Asp Leu
 115 120 125

25

Val Arg Phe Val Lys Gln Glu Glu Thr Ile Leu Ser Ser Ile Lys Val
 130 135 140

30

Thr Ile Asn Gln Gln Gly Ile Pro Glu Ala Gln Pro Asp Ser Met His
 145 150 155 160

35

Pro Val Ile Arg Lys Glu Ile Leu Ala Glu Gln Ala Glu Pro Gly Phe
 165 170 175

35

Ile Asp Pro Asp Tyr Phe Asn Glu Thr Tyr Phe Pro Lys Gly Met Lys
 180 185 190

40

Val Tyr Gln Phe Thr Gln Lys Val Ser Val Ala Gly Leu Pro Asp Gly
 195 200 205

45

Pro Gly Arg Ser Thr Pro Phe Thr Gly Ala
 210 215

<210> 43
 <211> 2732
 <212> PRT
 <213> Escherichia coli
 <400> 43

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Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu
 1 5 10 15

55

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala

	20	25	30
5	Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly 35	40	45
10	Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His 50	55	60
	Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn 65	70	75
15	Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln 85	90	95
20	Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn 100	105	110
25	Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val 115	120	125
	Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr 130	135	140
30	Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr 145	150	155
35	Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val 165	170	175
	Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg 180	185	190
40	Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala 195	200	205
45	Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr 210	215	220
50	Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys 225	230	235
	Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile 245	250	255
55			

5

His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu
 250 265 270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr
 275 280 285

10

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly
 290 295 300

15

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser
 305 310 315 320

20

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys
 325 330 335

20

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys
 340 345 350

25

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln
 355 360 365

30

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala
 370 375 380

35

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu
 385 390 395 400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys
 405 410 415

40

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val
 420 425 430

45

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly
 435 440 445

50

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr
 450 455 460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser
 465 470 475 480

55

Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Thr Met His Leu Val Leu
 485 490 495

5

Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys Gly
 500 505 510

10

Leu Thr Val Ser Ala Thr Ser Ser Gly Lys Lys Ser Val Thr His Ser
 515 520 525

15

Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu Asp Gly Glu
 530 535 540

20

Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys Leu Ser Thr
 545 550 555 560

25

Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser Ile Asn Ala
 565 570 575

30

Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln Thr Met Val
 580 585 590

Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser Ser Ala Pro
 595 600 605

35

Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly Val Leu Val
 610 615 620

Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn Ser Gly Leu
 625 630 635 640

40

Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg Leu Asp Asn
 645 650 655

45

Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr Leu Asp Ile
 660 665 670

Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn Gly Leu Met
 675 680 685

50

Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile Ala Asp Thr
 690 695 700

55

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Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu Leu Gln Gly
 705 710 715 720
 5 Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln Gly Ser His
 725 730 735
 10 Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly Lys Thr Leu
 740 745 750
 Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val Gln Ala Asp
 755 760 765
 15 Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn Leu Thr Ala
 770 775 780
 20 Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met Ser Gln Gly
 785 790 795 800
 25 Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly Ser Leu Leu
 805 810 815
 Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp Asn Arg Gly
 820 825 830
 30 Thr Val Gln Gly Asn His Val Thr Ile Arg Gln-Asn Ser Val Thr Asn
 835 840 845
 35 Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala Ala Arg Met
 850 855 860
 40 Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser Leu Leu Thr
 865 870 875 880
 Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser Ser Gly His
 885 890 895
 45 Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu Ala Asn Ser
 900 905 910
 50 Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu Thr Gly Glu
 915 920 925
 Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly Glu Met Ala
 55

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	930	935	940
5	Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile Ala Lys Asn 945 950 955 960		
10	Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp Ile Thr Gly 965 970 975		
15	Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn Asn Gln Ala 980 985 990		
20	Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu Lys Ala Asp Ser 995 1000 1005		
25	Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val Thr Thr Ile Thr 1010 1015 1020		
30	Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln Gly Glu Thr Leu 1025 1030 1035		
35	Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg Ser Gly Gly Val 1040 1045 1050		
40	Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr Ala Thr Leu Ser 1055 1060 1065		
45	Asn Gln Ser Thr Ile Gln Gly Gly Gly Val Ser Leu Asn Ala 1070 1075 1080		
50	Thr Asp Arg Leu Gln Asn Asp Gly Lys Ile Leu Ser Gly Ser Asn 1085 1090 1095		
55	Leu Thr Leu Thr Ala Gln Val Leu Ala Asn Thr Gly Ser Gly Leu 1100 1105 1110		
60	Val Gln Ala Ala Thr Leu Leu Leu Asp Val Val Asn Thr Val Asn 1115 1120 1125		
65	Gly Gly Arg Val Leu Ala Thr Gly Ser Asp Val Lys Gly Thr Thr 1130 1135 1140		
70	Leu Asn Asn Thr Gly Thr Leu Gln Gly Ala Thr Leu Val Asn Tyr 1145 1150 1155		

His Thr Phe Ser Ser Gly Thr Leu Leu Gly Thr Ser Gly Leu Gly
 1160 1165 1170

5

Val Lys Gly Ser Ser Leu Leu Gln Asn Gly Thr Gly Arg Leu Tyr
 1175 1180 1185

10

Ser Ala Gly Asn Leu Leu Leu Asp Ala Gln Asp Phe Ser Gly Gln
 1190 1195 1200

15

Gly Gln Val Val Ala Thr Gly Asp Val Thr Leu Lys Leu Ile Ala
 1205 1210 1215

20

Ala Leu Thr Asn His Gly Thr Leu Ala Ala Gly Lys Thr Leu Ser
 1220 1225 1230

25

Val Thr Ser Gln Asn Ala Ile Thr Asn Gly Gly Val Met Gln Gly
 1235 1240 1245

30

Asp Ala Met Val Leu Gly Ala Gly Glu Ala Phe Thr Asn Asn Gly
 1250 1255 1260

35

Leu Thr Ala Gly Lys Gly Asn Ser Val Phe Ser Ala Gln Arg Leu
 1265 1270 1275

Phe Leu Asn Ala Pro Gly Ser Leu Gln Gly Gly Asp Val Ser
 1280 1285 1290

40

Leu Asn Ser Arg Ser Asp Ile Thr Ile Ser Gly Phe Thr Gly Thr
 1295 1300 1305

45

Ala Gly Ser Leu Thr Met Asn Val Ala Gly Thr Leu Leu Asn Ser
 1310 1315 1320

Ala Leu Ile Tyr Ala Gly Asn Asn Leu Lys Leu Phe Thr Asp Arg
 1325 1330 1335

50

Leu His Asn Gln His Gly Asp Ile Leu Ala Gly Asn Ser Leu Trp
 1340 1345 1350

Val Gln Lys Asp Ala Ser Gly Gly Ala Asn Thr Glu Ile Ile Asn
 1355 1360 1365

55

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Asn Ser Gly Asn Ile Glu Thr His Gln Gly Asp Ile Val Val Arg
 1370 1375 1380
 5
 Thr Gly His Leu Leu Asn Gln Arg Glu Gly Phe Ser Ala Thr Thr
 1385 1390 1395
 10
 Thr Thr Arg Thr Asn Pro Ser Ser Ile Gln Gly Met Gly Asn Ala
 1400 1405 1410
 15
 Leu Val Asp Ile Pro Leu Ser Leu Leu Pro Asp Gly Ser Tyr Gly
 1415 1420 1425
 Tyr Phe Thr Arg Glu Val Glu Asn Gln His Gly Thr Pro Cys Asn
 1430 1435 1440
 20
 Gly His Gly Ala Cys Asn Ile Thr Met Asp Thr Leu Tyr Tyr Tyr
 1445 1450 1455
 25
 Ala Pro Phe Ala Asp Ser Ala Thr Gln Arg Phe Leu Ser Ser Gln
 1460 1465 1470
 30
 Asn Ile Thr Thr Val Thr Gly Ala Asp Asn Pro Ala Gly Arg Ile
 1475 1480 1485
 Ala Ser Gly Arg Asn Leu Ser Ala Glu Ala Glu Arg Leu Glu Asn
 1490 1495 1500
 35
 Arg Ala Ser Phe Ile Leu Ala Asn Gly Asp Ile Ala Leu Ser Gly
 1505 1510 1515
 40
 Arg Glu Leu Ser Asn Gln Ser Trp Gln Thr Gly Thr Glu Asn Glu
 1520 1525 1530
 45
 Tyr Leu Val Tyr Arg Tyr Asp Pro Lys Thr Phe Tyr Gly Ser Tyr
 1535 1540 1545
 Ala Thr Gly Ser Leu Asp Lys Leu Pro Leu Leu Ser Pro Glu Phe
 1550 1555 1560
 50
 Glu Asn Asn Thr Ile Arg Phe Ser Leu Asp Gly Arg Glu Lys Asp
 1565 1570 1575

55

Tyr Thr Pro Gly Lys Thr Tyr Tyr Ser Val Ile Gln Ala Gly Gly
 1580 1585 1590
 5 Asp Val Lys Thr Arg Phe Thr Ser Ser Ile Asn Asn Gly Thr Thr
 1595 1600 1605
 10 Thr Ala His Ala Gly Ser Val Ser Pro Val Val Ser Ala Pro Val
 1610 1615 1620
 Leu Asn Thr Leu Ser Gln Gln Thr Gly Gly Asp Ser Leu Thr Gln
 1625 1630 1635
 15 Thr Ala Leu Gln Gln Tyr Glu Pro Val Val Val Gly Ser Pro Gln
 1640 1645 1650
 20 Trp His Asp Glu Leu Ala Gly Ala Leu Lys Asn Ile Ala Gly Gly
 1655 1660 1665
 25 Ser Pro Leu Thr Gly Gln Thr Gly Ile Ser Asp Asp Trp Pro Leu
 1670 1675 1680
 Pro Ser Gly Asn Asn Gly Tyr Leu Val Pro Ser Thr Asp Pro Asp
 1685 1690 1695
 30 Ser Pro Tyr Leu Ile Thr Val Asn Pro Lys Leu Asp Gly Leu Gly
 1700 1705 1710
 35 Gln Val Asp Ser His Leu Phe Ala Gly Leu Tyr Glu Leu Leu Gly
 1715 1720 1725
 40 Ala Lys Pro Gly Gln Ala Pro Arg Glu Thr Ala Pro Ser Tyr Thr
 1730 1735 1740
 Asp Glu Lys Gln Phe Leu Gly Ser Ser Tyr Phe Leu Asp Arg Leu
 1745 1750 1755
 45 Gly Leu Lys Pro Glu Lys Asp Tyr Arg Phe Leu Gly Asp Ala Val
 1760 1765 1770
 50 Phe Asp Thr Arg Tyr Val Ser Asn Ala Val Leu Ser Arg Thr Gly
 1775 1780 1785
 Ser Arg Tyr Leu Asn Gly Leu Gly Ser Asp Thr Glu Gln Met Arg
 55

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	1790	1795	1800
5	Tyr Leu Met Asp Asn Ala Ala Arg Gln Gln Lys Gly 1805		Leu Gly Leu 1815
	Glu Phe Gly Val Ala Leu Thr Ala Glu Gln Ile Ala Gln Leu Asp 1820	1825	1830
10	Gly Ser Ile Leu Trp Trp Glu Ser Val Thr Ile Asn Gly Gln Thr 1835	1840	1845
15	Val Met Val Pro Lys Leu Tyr Leu Ser Pro Glu Asp Ile Thr Leu 1850	1855	1860
20	His Asn Gly Ser Val Ile Ser Gly Asn Asn Val Gln Leu Ala Gly 1865	1870	1875
	Gly Asn Ile Thr Asn Ser Gly Gly Ser Ile Asn Ala Gln Asn Asp 1880	1885	1890
25	Leu Ser Leu Asp Ser Ser Gly Tyr Ile Asp Asn Leu Asn Ala Gly 1895	1900	1905
30	Leu Ile Ser Ala Gly Gly Ser Leu Asp Leu Ser Ala Ile Gly Asp 1910	1915	1920
35	Ile Ser Asn Ile Ser Ser Val Ile Ser Gly Lys Thr Val Gln Leu 1925	1930	1935
	Glu Ser Val Ser Gly Asn Ile Ser Asn Ile Thr Arg Arg Gln Gln 1940	1945	1950
40	Trp Asn Ala Gly Ser Asp Ser Gln Tyr Gly Gly Val His Leu Ser 1955	1960	1965
45	Gly Thr Asp Thr Gly Pro Val Ala Thr Ile Lys Gly Thr Asp Ser 1970	1975	1980
50	Leu Ser Leu Asp Ala Gly Lys Asn Ile Asp Ile Thr Gly Ala Thr 1985	1990	1995
	Val Ser Ser Gly Gly Asp Leu Gly Met Ser Ala Gly Asn Asp Ile 2000	2005	2010

55

Asn Ile Ala Ala Asn Leu Ile Ser Gly Ser Lys Ser Gln Ser Gly
 2015 2020 2025

5

Phe Trp His Thr Asp Asp Asn Ser Ser Ser Ser Thr Thr Ser Gln
 2030 2035 2040

10

Gly Ser Ser Ile Ser Ala Gly Gly Asn Leu Ala Met Ala Ala Gly
 2045 2050 2055

15

His Asn Leu Asp Val Thr Ala Ser Ser Val Ser Ala Gly His Ser
 2060 2065 2070

20

Ala Leu Leu Ser Cys Arg Ser Arg Pro Ser Leu Glu Cys Ser Gln
 2075 2080 2085

Gly Lys Ala Lys Thr Ser Arg Asn Gly Arg Ser Glu Ser His Glu
 2090 2095 2100

25

Ser His Ala Ala Val Ser Thr Val Thr Ala Gly Asp Asn Phe Leu
 2105 2110 2115

30

Leu Val Ala Gly Arg Asp Ile Ala Ser Gln Ala Ala Gly Met Ala
 2120 2125 2130

35

Ala Glu Asn Asn Val Val Ile Arg Gly Gly Arg Asp Val Asn Leu
 2135 2140 2145

40

Val Ala Glu Ser Ala Gly Ala Gly Asp Ser Tyr Thr Ser Lys Lys
 2150 2155 2160

Lys Lys Glu Ile Asn Glu Thr Val Arg Gln Gln Gly Thr Glu Ile
 2165 2170 2175

45

Ala Ser Gly Gly Asp Thr Thr Val Asn Ala Gly Arg Asp Ile Thr
 2180 2185 2190

50

Ala Val Ala Ser Ser Val Thr Ala Thr Gly Asn Ile Ser Val Asn
 2195 2200 2205

Ala Gly Arg Asp Val Ala Leu Thr Thr Ala Thr Glu Ser Asp Tyr
 2210 2215 2220

55

His Tyr Leu Glu Thr Lys Lys Lys Ser Gly Gly Phe Leu Ser Lys
 2225 2230 2235

5 Lys Thr Thr Arg Thr Ile Ser Glu Asp Ser Ala Thr Arg. Glu Ala
 2240 2245 2250

10 Gly Ser Leu Leu Ser Gly Asn Arg Val Thr Val Asn Ala Gly Asp
 2255 2260 2265

15 Asn Leu Thr Val Glu Gly Ser Asp Val Val Ala Asp Arg Asp Val
 2270 2275 2280

Ser Leu Ala Ala Gly Asn His Val Asp Val Leu Ala Ala Thr Ser
 2285 2290 2295

20 Thr Asp Thr Ser Trp Arg Phe Lys Glu Thr Lys Lys Ser Gly Leu
 2300 2305 2310

25 Met Gly Thr Gly Gly Ile Gly Phe Thr Ile Gly Ser Ser Lys Thr
 2315 2320 2325

30 Thr His Asp Arg Arg Glu Ala Gly Thr Thr Gln Ser Gln Ser Ala
 2330 2335 2340

Ser Thr Ile Gly Ser Thr Ala Gly Asn Val Ser Ile Thr Ala Gly
 2345 2350 2355

35 Lys Gln Ala His Ile Ser Gly Ser Asp Val Ile Ala Asn Arg Asp
 2360 2365 2370

40 Ile Ser Ile Thr Gly Asp Ser Val Val Val Asp Pro Gly His Asp
 2375 2380 2385

45 Arg Arg Thr Val Asp Glu Lys Phe Glu Gln Lys Lys Ser Gly Leu
 2390 2395 2400

Thr Val Ala Leu Ser Gly Thr Val Gly Ser Ala Ile Asn Asn Ala
 2405 2410 2415

50 Val Thr Ser Ala Gln Glu Thr Lys Glu Ser Ser Asp Ser Arg Leu
 2420 2425 2430

55

Lys Ala Leu Gln Ala Thr Lys Thr Ala Leu Ser Gly Val Gln Ala
 2435 2440 2445

5 Gly Gln Ala Ala Thr Met Ala Ser Ala Thr Gly Asp Pro Asn Ala
 2450 2455 2460

10 Gly Val Ser Leu Ser Leu Thr Thr Gln Lys Ser Lys Ser Gln Gln
 2465 2470 2475

His Ser Glu Ser Asp Thr Val Ser Gly Ser Thr Leu Asn Ala Gly
 2480 2485 2490

15 Asn Asn Leu Ser Val Val Ala Thr Gly Lys Asn Arg Gly Asp Asn
 2495 2500 2505

20 Arg Gly Asp Ile Val Ile Ala Gly Ser Gln Leu Lys Ala Gly Gly
 2510 2515 2520

25 Asn Thr Ser Leu Asp Ala Ala Asn Asp Ile Leu Leu Ser Gly Ala
 2525 2530 2535

Ala Asn Thr Gln Lys Thr Thr Gly Arg Asn Ser Ser Ser Gly Gly
 2540 2545 2550

30 Gly Val Gly Val Ser Ile Gly Ala Gly Lys Gly Ala Gly Ile Ser
 2555 2560 2565

35 Ala Phe Ala Ser Val Asn Ala Ala Lys Gly Arg Glu Lys Gly Asn
 2570 2575 2580

40 Gly Thr Thr Thr Asp Lys Thr Val Thr Ile Asn Ser Gly Arg Asp
 2585 2590 2595

Thr Val Leu Asn Gly Ala Gln Val Asn Gly Asn Arg Ile Ile Ala
 2600 2605 2610

45 Asp Val Gly His Asp Leu Leu Ile Ser Ser Gln Gln Asp Thr Ser
 2615 2620 2625

50 Lys Tyr Asp Ser Lys Gln Thr Ser Val Ala Ala Gly Gly Ser Phe
 2630 2635 2640

55 Thr Phe Gly Ser Met Thr Gly Ser Gly Tyr Ile Ala Ala Ser Arg

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	2645	2650	2655	
5	Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr Gly 2660	2665	2670	
10	Met Phe Ala Arg Val Met Val Ala Ser Thr Ser Gln Trp Val Asn 2675	2680	2685	
15	Ile Pro Asn Trp Met Val Arg Ser Leu Pro His Cys His Thr Gly 2690	2695	2700	
20	Glu Lys Pro Pro Gly Tyr Arg Thr Leu Gly Leu Val Thr Leu Gln 2705	2710	2715	
25	Arg Ser Gly Ile Ile Lys Ser Ser His Arg Trp Asn Gln Ser 2720	2725	2730	
	<210> 44			
	<211> 321			
	<212> PRT			
	<213> Escherichia coli			
	<400> 44			
30	Met Met Leu Lys Lys Thr Ile Phe Ile Leu Thr Leu Phe Ser Gly Asn 1	5	10	15
	Val Ile Ala Ala Thr Val Glu Leu Gly Phe Glu Asn Glu Gln Tyr Asn 20	25	30	
35	Tyr Ala Tyr Arg Ser Ala Asp Val Phe Met Pro Tyr Ile Lys Ser Asn 35	40	45	
40	Phe Asn Pro Val Thr Asp Ser Ala Leu Asn Val Ser Leu Thr Tyr Met 50	55	60	
45	Tyr Gln Asp Gln Tyr Gly Lys Lys His Lys Lys Thr Ser Glu Asp Arg 65	70	75	80
	Phe Lys Thr Asn Arg Asp Arg Ile Glu Leu Tyr Leu Lys Gly Tyr Thr 85	90	95	
50	Leu Asn Arg Gly Ala Tyr Ser Phe Ser Pro Ser Ala Gly Phe Arg Tyr 100	105	110	

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Glu Ser Trp Asp Val Asn Tyr Asp Asn Pro Lys Lys Gln Asp Lys Trp
 115 120 125

5 Lys Leu Glu Leu Arg Phe Tyr Pro Asn Met Thr Tyr Lys Leu Asn Asp
 130 135 140

10 Gln Leu Ser Leu Tyr Met Asn Gly Phe Val Ala Pro Val Phe Phe Lys
 145 150 155 160

15 Thr Gln Gln Glu Ser Arg Lys Asp Asn Asn Tyr Val Lys Gly Lys Leu
 165 170 175

180 Gly Ala Lys Arg Tyr Asn Asn Asp Tyr Tyr Gln Glu Leu Gln Ile Leu
 185 190

20 Gly Val Arg Tyr Lys Phe Asn Asn Asp Asn Thr Leu Trp Ala Ser Val
 195 200 205

25 Tyr Asn Glu Arg Lys Tyr Asn Gln His Ser Ser Lys Tyr Asp Arg Trp
 210 215 220

225 Gln Leu Arg Gly Gly Tyr Asp Phe Lys Val Thr Glu Glu Phe Val Leu
 230 235 240

30 Ser Pro Phe Ile Arg Tyr Asp Leu Ser Tyr Arg Glu Lys Asn Leu Glu
 245 250 255

35 Ser Thr Ser Asn Asn Gly Leu Ser Lys Asn Asn Lys Glu Ile Arg Thr
 260 265 270

40 Gly Ala Ser Phe Ser Tyr Lys Ile Ile Pro Ser Val Lys Leu Val Gly
 275 280 285

45 Glu Ile Tyr Arg Gln Thr Thr Asn Ile Glu Asn Tyr Tyr Gly Glu His
 290 295 300

50 Ser Glu Asp Lys Asn Arg Met Phe Tyr Lys Leu Gly Ile Asn Lys Thr
 305 310 315 320

Phe

<210> 45

55

<211> 587

<212> PRT

<213> Escherichia coli

<400> 45

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Met	Gln	His	Arg	Gln	Lys	Asn	Ile	Leu	Thr	Lys	Thr	Ser	Leu	Leu	Ser
							5			10					
															15

10

Arg	Ala	Leu	Ser	Val	Pro	Cys	Cys	Asp	Met	Phe	Arg	Arg	Gly	Ser	Pro
										25					30

15

Trp	Ile	Cys	Tyr	Leu	Ser	Leu	Ser	Val	Phe	Ser	Gly	Cys	Phe	Ile	Pro
							35			40					45

20

Ala	Phe	Ser	Ser	Pro	Ala	Ala	Met	Leu	Ser	Pro	Gly	Asp	Arg	Ser	Ala
						50		55			60				

25

Ile	Gln	Gln	Gln	Gln	Gln	Gln	Leu	Leu	Asp	Glu	Asn	Gln	Arg	Gln	Arg
						65		70		75			80		

30

Asp	Ala	Leu	Glu	Arg	Pro	Leu	Thr	Ile	Thr	Pro	Ser	Pro	Glu	Thr	Ser
						85			90				95		

35

Ala	Gly	Thr	Glu	Gly	Pro	Cys	Phe	Thr	Val	Ser	Ser	Ile	Val	Val	Ser
						100		105					110		

40

Gly	Ala	Thr	Arg	Leu	Thr	Ser	Ala	Glu	Thr	Asp	Arg	Leu	Val	Pro	Trp
						115		120			125				

45

Val	Asn	Gln	Cys	Leu	Asn	Ile	Thr	Gly	Leu	Thr	Ala	Val	Thr	Asp	Ala
					130		135			140					

50

Val	Thr	Asp	Gly	Tyr	Ile	Arg	Arg	Gly	Tyr	Ile	Thr	Ser	Arg	Ala	Phe
					145		150			155			160		

55

Leu	Thr	Glu	Gln	Asp	Leu	Ser	Gly	Gly	Val	Leu	His	Ile	Thr	Val	Met
					165		170				175				

55

Glu	Gly	Arg	Leu	Gln	Gln	Ile	Arg	Ala	Glu	Gly	Ala	Asp	Leu	Pro	Ala
					180		185				190				

55

Arg	Thr	Leu	Lys	Met	Val	Phe	Pro	Gly	Met	Glu	Gly	Lys	Val	Leu	Asn
					195		200			205					

Leu Arg Asp Ile Glu Gln Gly Met Glu Gln Ile Asn Arg Leu Arg Thr
 210 215 220

5 Glu Pro Val Gln Ile Glu Ile Ser Pro Gly Asp Arg Glu Gly Trp Ser
 225 230 235 240

10 Val Val Thr Leu Thr Ala Leu Pro Glu Trp Pro Val Thr Gly Ser Val
 245 250 255

Gly Ile Asp Asn Ser Gly Gln Lys Ser Thr Gly Thr Gly Gln Leu Asn
 260 265 270

15 Gly Val Leu Ser Phe Asn Asn Pro Leu Gly Leu Ala Asp Asn Trp Phe
 275 280 285

20 Val Ser Gly Gly Arg Ser Ser Asp Phe Ser Val Ser His Asp Ala Arg
 290 295 300

25 Asn Phe Ala Ala Gly Val Ser Leu Pro Tyr Gly Tyr Thr Leu Val Asp
 305 310 315 320

Tyr Thr Tyr Ser Trp Ser Asp Tyr Leu Ser Thr Ile Asp Asn Arg Gly
 325 330 335

30 Trp Arg Trp Arg Ser Thr Gly Asp Leu Gln Thr His Arg Leu Gly Leu
 340 345 350

35 Ser His Val Leu Phe Arg Asn Gly Asp Met Lys Thr Ala Leu Thr Gly
 355 360 365

40 Gly Leu Gln His Arg Ile Ile His Asn Tyr Leu Asp Asp Val Leu Leu
 370 375 380

Gln Gly Ser Ser Arg Lys Leu Thr Ser Phe Ser Val Gly Leu Asn His
 385 390 395 400

45 Thr His Lys Phe Leu Gly Gly Val Gly Thr Leu Asn Pro Val Phe Thr
 405 410 415

50 Arg Gly Met Pro Trp Phe Gly Ala Glu Ser Asp His Gly Lys Arg Gly
 420 425 430

Asp Leu Pro Val Asn Gln Phe Arg Lys Trp Ser Val Ser Ala Ser Phe

55

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435

440

445

5 Gln Arg Pro Val Thr Asp Arg Val Trp Trp Leu Thr Ser Ala Tyr Ala
450 455 460

10 Gln Trp Ser Pro Asp Arg Leu His Gly Val Glu Gln Leu Ser Leu Gly
465 470 475 480

Gly Glu Ser Ser Val Arg Gly Phe Lys Asp Gln Tyr Ile Ser Gly Asn
485 490 495

15 Asn Gly Gly Tyr Leu Arg Asn Glu Leu Ser Trp Ser Leu Phe Ser Leu
500 505 510

20 Pro Tyr Val Gly Thr Val Arg Ala Val Ala Ala Leu Asp Gly Gly Trp
515 520 525

25 Leu His Ser Asp Ser Asp Asp Pro Tyr Ser Ser Gly Thr Leu Trp Gly
530 535 540

30 Ala Ala Ala Gly Leu Ser Thr Thr Ser Gly His Val Ser Gly Ser Phe
545 550 555 560

35 Thr Ala Gly Leu Pro Leu Val Tyr Pro Asp Trp Leu Ala Pro Asp His
565 570 575

Leu Thr Val Tyr Trp Arg Val Ala Val Ala Phe
580 585

40 <210> 46
<211> 744
<212> PRT
<213> Escherichia coli
<400> 46

45 Met Asn Lys His Thr Leu Leu Leu Thr Val Leu Phe Leu Asn Leu Ile
1 5 10 15

45 Cys Thr Pro Val Phe Ala Gln Asn Trp Gln Val Ala Thr Phe Gly Gln
20 25 30

50 Ser Thr Asp Leu Asn Phe Ser Ser Leu Ile Asp Ser Ala Lys Ile Gly
35 40 45

55

Arg Asn Asn Ala Trp Leu Ala Gly Asn Asn Asn Phe Leu Glu Ala Gly
 50 55 60

5 Lys Phe Tyr Thr Leu Pro Thr Asp Phe Phe Ile Glu Ser Arg Gly Gly
 65 70 75 80

10 Lys Ile Ala Asn Ser His Asp Gly Met Thr Val Phe Tyr Thr Ile Val
 85 90 95

15 Pro Val Thr Gln Thr Phe Arg Leu Glu Ala Asp Leu Thr Leu Glu Gln
 100 105 110

Ile Gly Pro Glu Val Asn Gly Lys Ser Pro Ala Gly Gln Glu Gly Ala
 115 120 125

20 Gly Leu Phe Val Arg Asp Ile Ile Gly Pro Gln Arg Gln Glu Pro Gln
 130 135 140

25 Ser Ala Gly Thr Glu Glu Tyr Pro Gln Ala Ser Asn Ile Leu Met Asn
 145 150 155 160

Ala Phe Ile Thr Gln Asn Lys Lys Asn Asn Leu Val Gln Ile Thr
 165 170 175

30 Ser Ile Val Arg Glu Gly Val Ile Lys Thr Trp Gly Asn Glu Gly Ile
 180 185 190

35 Thr Ile Lys Lys Gln Pro Ile Ile Glu Asn Ile Asn Phe Thr Gln Lys
 195 200 205

40 Arg Asn Ile His Met Thr Ile Glu Arg Leu Pro Glu Lys Phe Ile Leu
 210 215 220

Thr Ala Phe Asp Thr Asp Arg Lys Glu Asn Gln Ser Trp Gln Phe Ser
 225 230 235 240

45 Asp Tyr Ser Gly Phe Met Asn Gln Leu Asp Asn Asn Ser Leu Ala Ile
 245 250 255

50 Gly Phe Phe Ala Ala Arg Asn Ala Lys Leu Arg Val Lys Asn Ala Ser
 260 265 270

Phe Lys Pro Gly Lys Pro Leu Val Asp Tyr Lys Gln Leu Thr Ser Arg

55

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5

Ala Lys Asp Lys Asn Arg Phe Phe Trp Pro Ala His Asn Leu Val Leu
 515 520 525

Asn Ser Asp Ser Tyr Asn Asn Leu Asp Leu Ser Gly Ile Asn Ala Asp
 530 535 540

10

Gly Phe Ala Ala Lys Leu Gly Val Gly Pro Gly Asn Ile Phe Arg Gly
 545 550 555 560

15

Cys Ile Ala His Asn Asn Ala Asp Asp Gly Trp Asp Leu Phe Asn Lys
 565 570 575

20

Ile Glu Asp Gly Pro Asn Ala Ser Val Thr Ile Glu Asn Ser Val Ala
 580 585 590

25

Tyr Glu Asn Gly Leu Pro Tyr Asn Lys Ala Asp Ile Leu Lys Gly Ser
 595 600 605

30

Ile Gly Asn Gly Gly Glu Gly Gln Pro Ser Lys Ser Gln Val Ile Asn
 610 615 620

Ser Ile Ala Ile Asn Asn Asn Met Asp Gly Phe Thr Asp Asn Phe Asn
 625 630 635 640

35

Thr Gly Ser Leu Ile Val Arg Asn Asn Ile Ala Met Asn Asn Ala Arg
 645 650 655

40

Tyr Asn Tyr Ile Leu Arg Thr Asn Pro Tyr Lys Phe Pro Ser Ser Ile
 660 665 670

Leu Phe Asp Asn Asn Tyr Ser Ile Arg Asp Asp Trp Glu Asn Lys Ile
 675 680 685

45

Lys Asp Phe Leu Gly Asp Thr Val Asn Ser Val Asn Tyr Lys Leu Leu
 690 695 700

Val Ser His Glu Thr Gly Pro Val Gln Lys Asp Leu Phe Phe Thr Arg
 705 710 715 720

50

Asp Asp Ser Gly Asn Ile Ile Tyr Pro Asp Phe Phe Leu Asn Ile Ile
 725 730 735

55

Asn Lys Phe Asn Glx Thr Met Pro
740

5

<210> 47
<211> 136
<212> PRT
<213> Escherichia coli
<400> 47

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Met Lys Thr Phe Ile Lys Thr Leu Leu Val Ala Val Thr Ile Leu Phe
1 5 10 15

15

Ser Val Phe Ala Thr Ala Lys Gln Val Lys Leu Pro Asn Asn Ile Lys
20 25 30

20

Tyr Val Asn Thr Thr Glu Ala Phe Ser Cys Thr Glu Ile Asp Gly Met
35 40 45

25

Asn Cys Gln Thr Lys Asn Pro Phe Asn Tyr Lys Asp Asn Ser Tyr Val
50 55 60

30

Val Leu Asn Leu Lys Thr Gly Lys Ala Gln Met Leu Glu Tyr Lys Asp
85 90 95

35

Asn Gln Leu Cys Ser Gly Ser Asn Lys Pro Phe Phe Glu Ile Lys Asn
100 105 110

40

Gly Val Pro Thr Val Gly Val Ile Asp Thr Ser Gly Lys Pro Val Val
115 120 125

Val Ala Leu Asp Lys Leu Lys Thr
130 135

45

<210> 48
<211> 225
<212> PRT
<213> Escherichia coli
<400> 48

50

Met Gln Leu Pro Val Lys Leu Leu Met Ser Leu Ile Ser Leu Val Ser
1 5 10 15

55

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Val Ile Ala Arg Ala Gly Lys Tyr Lys Asn Tyr Ile Arg Asp Glu Ile
20 25 30

5 Lys Tyr Trp Arg Tyr Thr Ser Tyr Lys Gly Gly Glu Phe Pro Glu Gly
35 40 45

10 Phe Thr Asp Glu Lys Phe Ser Ser Ala Ile Tyr Asn Gly Arg Ile Phe
50 55 60

Thr Met Lys Arg Leu His Thr Leu Met Leu Phe Leu Ala Val Leu Phe
65 70 75 80

15 Thr Gly Phe Asn Val Glu Ala Ala Ser Val Lys Gln Ala Leu Ser Cys
85 90 95

20 Asp Pro Asn Ala Arg Ala Glu Gln Pro Gly Ala Cys Pro Thr Thr Tyr
100 105 110

25 Glu Leu Tyr Glu Gly Asp Ala Ala Tyr Lys Ala Ala Leu Asp Lys Ala
115 120 125

Leu Lys Pro Val Gly Leu Ser Gly Met Phe Gly Lys Gly Gly Tyr Met
130 135 140

30 Asp Gly Pro Gly Gly Asn Val Thr Pro Val Thr Ile Asn Gly Thr Val
145 150 155 160

35 Trp Leu Gln Gly Asp Gly Cys Lys Ala Asn Thr Cys Gly Trp Asp Phe
165 170 175

40 Ile Val Thr Leu Tyr Asn Pro Lys Thr His Glu Val Val Gly Tyr Arg
180 185 190

Tyr Phe Gly Leu Asp Asp Pro Ala Tyr Leu Val Trp Phe Gly Glu Ile
195 200 205

45 Gly Val His Glu Phe Ala Tyr Leu Val Lys Asn Tyr Val Ala Ala Val
210 215 220

50 Asn
225

<210> 49

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<211> 721
 <212> PRT
 <213> Escherichia coli
 <400> 49

5 Met Lys Thr Gln Ile Thr Phe Ala Ala Leu Leu Pro Ala Leu Ala Ser
 1 5 10 15

10 Phe Ile Pro Leu His Ala His Ala Ser Ser Thr Ser Glu Asp Glu Met
 20 25 30

15 Ile Val Thr Gly Asn Thr Ala Ala Asp Thr Thr Asp Ser Ala Ala Gly
 35 40 45

Ala Gly Phe Lys Thr Asn Asp Ile Asp Val Gly Pro Leu Gly Thr Lys
 50 55 60

20 Ser Trp Ile Glu Thr Pro Tyr Ser Ser Thr Thr Val Thr Lys Glu Met
 65 70 75 80

25 Ile Glu Asn Gln Gln Ala Gln Ser Val Ser Glu Met Leu Lys Tyr Ser
 85 90 95

30 Pro Ser Thr Gln Met Gln Ala Arg Gly Gly Met Asp Val Gly Arg Pro
 100 105 110

Gln Ser Arg Gly Met Gln Gly Ser Val Val Ala Asn Ser Arg Leu Asp
 115 120 125

35 Gly Leu Asn Ile Val Ser Thr Thr Ala Phe Pro Val Glu Met Leu Glu
 130 135 140

40 Arg Met Asp Val Leu Asn Ser Leu Thr Gly Ala Leu Tyr Gly Pro Ala
 145 150 155 160

45 Ser Pro Ala Gly Gln Phe Asn Phe Val Ala Lys Arg Pro Thr Glu Glu
 165 170 175

Thr Leu Arg Lys Val Thr Leu Gly Tyr Gln Ser Arg Ser Ala Phe Thr
 180 185 190

50 Gly His Ala Asp Leu Gly Gly His Phe Asp Glu Asn Lys Arg Phe Gly
 195 200 205

55

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Tyr Arg Val Asn Leu Leu Asp Gln Glu Gly Glu Gly Asn Val Asp Asp
210 215 220

5 Ser Thr Leu Arg Arg Lys Leu Val Ser Val Ala Leu Asp Trp Asn Ile
225 230 235 240

10 Gln Pro Gly Thr Gln Leu Gln Leu Asp Ala Ser His Tyr Glu Phe Ile
245 250 255

Gln Lys Gly Tyr Val Gly Ser Phe Asn Tyr Gly Pro Asn Val Lys Leu
260 265 270

15 Pro Ser Ala Pro Asn Pro Lys Asp Lys Asn Leu Ala Leu Ser Thr Ala
275 280 285

20 Gly Asn Asp Leu Thr Thr Asp Thr Ile Ser Thr Arg Leu Ile His Tyr
290 295 300

25 Phe Asn Asp Asp Trp Ser Met Asn Ala Gly Val Gly Trp Gln Gln Ala
305 310 315 320

Asp Arg Ala Met Arg Ser Val Ser Ser Lys Ile Leu Asn Asn Gln Gly
325 330 335

30 Asp Ile Ser Arg Ser Met Lys Asp Ser Thr Ala Ala Gly Arg Phe Arg
340 345 350

35 Val Leu Ser Asn Thr Ala Gly Leu Asn Gly His Ile Asp Thr Gly Ser
355 360 365

Ile Gly His Asp Leu Ser Leu Ser Thr Thr Gly Tyr Val Trp Ser Leu
370 375 380

40 Tyr Ser Ala Lys Gly Thr Gly Ser Ser Tyr Ser Trp Gly Thr Thr Asn
385 390 395 400

45 Met Tyr His Pro Asp Ala Ile Asp Glu Gln Gly Asp Gly Lys Ile Arg
405 410 415

50 Thr Gly Gly Pro Arg Tyr Arg Ser Ser Val Asn Thr Gln Gln Ser Val
420 425 430

55 Thr Leu Gly Asp Thr Val Thr Phe Thr Pro Gln Trp Ser Ala Met Phe

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	435	440	445
5	Tyr Leu Ser Gln Ser Trp Leu Gln Thr Lys Asn Tyr Asp Lys His Gly 450	455	460
	Asn Gln Thr Asn Gln Val Asp Glu Asn Gly Leu Ser Pro Asn Ala Ala 465		
10	Leu Met Tyr Lys Ile Thr Pro Asn Thr Met Ala Tyr Val Ser Tyr Ala 485		
	490		
15	Asp Ser Leu Glu Gln Gly Gly Thr Ala Pro Thr Asp Glu Ser Val Lys 500		
	505		
20	Asn Ala Gly Gln Thr Leu Asn Pro Tyr Arg Ser Lys Gln Tyr Glu Val 515		
	520		
	Gly Leu Lys Ser Asp Ile Gly Glu Met Asn Leu Gly Ala Ala Leu Phe 530		
25	535		
	Arg Leu Glu Arg Pro Phe Ala Tyr Leu Asp Thr Asp Asn Val Tyr Lys 545		
	550		
30	Glu Gln Gly Asn Gln Val Asn Asn Gly Leu Glu Leu Thr Ala Ala Gly 565		
	570		
	Asn Val Trp Gln Gly Leu Asn Ile Tyr Ser Gly Val Thr Phe Leu Asp 580		
35	585		
	590		
	Pro Lys Leu Lys Asp Thr Ala Asn Ala Ser Thr Ser Asn Lys Gln Val 595		
	600		
40	Val Gly Val Pro Lys Val Gln Ala Asn Leu Leu Ala Glu Tyr Ser Leu 610		
	615		
	620		
45	Pro Ser Ile Pro Glu Trp Val Tyr Ser Ala Asn Val His Tyr Thr Gly 625		
	630		
	635		
50	Lys Arg Ala Ala Asn Asp Thr Asn Thr Ser Tyr Ala Ser Ser Tyr Thr 645		
	650		
	655		
	Thr Trp Asp Leu Gly Thr Arg Tyr Thr Thr Lys Val Ser Asn Val Pro 660		
	665		
	670		
55			

Thr Thr Phe Arg Val Val Val Asn Asn Val Phe Asp Lys His Tyr Trp
675 680 685

5

Ala Ser Ile Phe Pro Ser Gly Thr Asp Gly Asp Asn Gly Ser Pro Ser
690 695 700

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Ala Phe Ile Gly Gly Arg Glu Val Arg Ala Ser Val Thr Phe Asp
705 710 715 720

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Phe

<210> 50

<211> 669

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<212> PRT

<213> Escherichia coli

<400> 50

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Met Lys Asn Ile Thr Leu Trp Gln Arg Leu Arg Gln Val Ser Ile Ser
1 5 10 15

Thr Ser Leu Arg Cys Ala Phe Leu Met Gly Ala Leu Leu Thr Leu Ile
20 25 30

30

Val Ser Ser Val Ser Leu Tyr Ser Trp His Glu Gln Ser Ser Gln Ile
35 40 45

35

Arg Tyr Ser Leu Asp Lys Tyr Phe Pro Arg Ile His Ser Ala Phe Leu
50 55 60

40

Ile Glu Gly Asn Leu Asn Leu Val Val Asp Gln Leu Asn Glu Phe Leu
65 70 75 80

Gln Ala Pro Asn Thr Thr Val Arg Leu Gln Leu Arg Thr Gln Ile Ile
85 90 95

45

Gln His Leu Asp Thr Ile Glu Arg Leu Ser Arg Gly Leu Ser Ser Arg
100 105 110

50

Glu Arg Gln Gln Leu Thr Val Ile Leu Gln Asp Ser Arg Ser Leu Leu
115 120 125

Ser Glu Leu Asp Arg Ala Leu Tyr Asn Met Phe Leu Leu Arg Glu Lys

55

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	130	135	140
5	Val Ser Glu Leu Ser Ala Arg Ile Asp Trp Leu His Asp Asp Phe Thr 145 150 155 160		
	Thr Glu Leu Asn Ser Leu Val Gln Asp Phe Thr Trp Gln Gln Gly Thr 165 170 175		
10	Leu Leu Asp Glu Ile Ala Ser Arg Gln Gly Asp Thr Ala Gln Tyr Leu 180 185 190		
15	Lys Arg Ser Arg Glu Val Gln Asn Glu Gln Gln Val Tyr Thr Leu 195 200 205		
20	Ala Arg Ile Glu Asn Gln Ile Val Asp Asp Leu Arg Asp Arg Leu Asn 210 215 220		
	Glu Leu Lys Ser Gly Arg Asp Asp Asp Ile Gln Val Glu Thr His Leu 225 230 235 240		
25	Arg Tyr Phe Glu Asn Leu Lys Lys Thr Ala Asp Glu Asn Ile Arg Met 245 250 255		
30	Leu Asp Asp Trp Pro Gly Thr Ile Leu Arg Gln Thr Ile Asp Glu 260 265 270		
35	Leu Leu Asp Met Gly Ile Val Lys Asn Lys Met Pro Asp Thr Met Arg 275 280 285		
	Glu Tyr Val Ala Ala Gln Lys Ala Leu Glu Asp Ala Ser Arg Thr Arg 290 295 300		
40	Glu Ala Thr Gln Gly Arg Phe Arg Thr Leu Leu Glu Ala Gln Leu Gly 305 310 315 320		
45	Ser Thr His Gln Gln Met Gln Met Phe Asn Gln Arg Met Glu Gln Ile 325 330 335		
50	Val His Val Ser Gly Gly Leu Ile Leu Val Ala Thr Ala Leu Ala Leu 340 345 350		
	Leu Leu Ala Trp Val Phe Asn His Tyr Phe Ile Arg Ser Arg Leu Val 355 360 365		
55			

5

Lys Arg Phe Thr Leu Leu Asn Gln Ala Val Val Gln Ile Gly Leu Gly
 370 375 380

Gly Thr Glu Thr Thr Ile Pro Val Tyr Gly Asn Asp Glu Leu Gly Arg
 385 390 395 400

10

Ile Ala Gly Leu Leu Arg His Thr Leu Gly Gln Leu Asn Val Gln Lys
 405 410 415

15

Gln Gln Leu Glu Gln Glu Ile Thr Asp Arg Lys Val Ile Glu Ala Asp
 420 425 430

20

Leu Arg Ala Thr Gln Asp Glu Leu Ile Gln Thr Ala Lys Leu Ala Val
 435 440 445

25

Val Gly Gln Thr Met Thr Thr Leu Ala His Glu Ile Asn Gln Pro Leu
 450 455 460

30

Asn Ala Leu Ser Met Tyr Leu Phe Thr Ala Arg Arg Ala Ile Glu Gln
 465 470 475 480

35

Thr Gln Lys Glu Gln Ala Ser Met Met Leu Gly Lys Ala Glu Gly Val
 485 490 495

Ile Ser Arg Ile Asp Ala Ile Ile Arg Ser Leu Arg Gln Phe Thr Arg
 500 505 510

40

Arg Ala Glu Leu Glu Thr Ser Leu His Ala Val Asp Leu Ala Gln Met
 515 520 525

45

Phe Ser Ala Ala Trp Glu Leu Leu Ala Met Arg His Arg Ser Leu Gln
 530 535 540

50

Ala Thr Leu Val Leu Pro Gln Gly Thr Ala Thr Val Ser Gly Asp Glu
 545 550 555 560

Val Arg Thr Gln Gln Val Leu Val Asn Val Leu Ala Asn Ala Leu Asp
 565 570 575

55

Val Cys Gly Gln Gly Ala Val Ile Thr Val Asn Trp Gln Met Gln Gly
 580 585 590

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Lys Thr Leu Asn Val Phe Ile Gly Asp Asn Gly Pro Gly Trp Pro Glu
595 600 605

5 Ala Leu Leu Pro Ser Leu Leu Lys Pro Phe Thr Thr Ser Lys Glu Val
610 615 620

10 Gly Leu Gly Ile Gly Leu Ser Ile Cys Val Ser Leu Met Glu Gln Met
625 630 635 640

15 Lys Gly Glu Leu Arg Leu Ala Ser Thr Met Thr Arg Asn Ala Cys Val
645 650 655

20 Val Leu Gln Phe Arg Leu Thr Asp Val Glu Asp Ala Lys
660 665

25 <210> 51
<211> 753
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<400> 51

Met Asn Val Ile Lys Leu Ala Ile Gly Ser Gly Ile Leu Leu Ser
1 5 10 15

30 Cys Gly Ala Tyr Ser Gln Ser Ile Ser Glu Lys Thr Asn Ser Asp Lys
20 25 30

35 Lys Gly Ala Ala Glu Phe Ser Pro Leu Ser Val Ser Val Gly Lys Thr
35 40 45

40 Thr Ser Glu Gln Glu Ala Leu Glu Lys Thr Gly Ala Thr Ser Ser Arg
50 55 60

45 Thr Thr Asp Lys Asn Leu Gln Ser Leu Asp Ala Thr Val Arg Ser Met
65 70 75 80

50 Pro Gly Thr Tyr Thr Gln Ile Asp Pro Gly Gln Gly Ala Ile Ser Val
85 90 95

55 Asn Ile Arg Gly Met Ser Gly Phe Gly Arg Val Asn Thr Met Val Asp
100 105 110

Gly Ile Thr Gln Ser Phe Tyr Gly Thr Ser Thr Ser Gly Thr Thr Thr
115 120 125

55

His Gly Ser Thr Asn Asn Met Ala Gly Val Leu Ile Asp Pro Asn Leu
 130 135 140

5
 Leu Val Ala Val Asp Val Thr Arg Gly Asp Ser Ser Gly Ser Glu Gly
 145 150 155 160

10 Ile Asn Ala Leu Ala Gly Ser Ala Asn Met Arg Thr Ile Gly Val Asp
 165 170 175

15 Asp Val Ile Phe Asn Gly Asn Thr Tyr Gly Leu Arg Ser Arg Phe Ser
 180 185 190

20 Val Gly Ser Asn Gly Leu Gly Arg Ser Gly Met Ile Ala Leu Gly Gly
 195 200 205

Lys Ser Asp Ala Phe Thr Asp Thr Gly Ser Ile Gly Val Met Ala Ala
 210 215 220

25 Val Ser Gly Ser Ser Val Tyr Ser Asn Phe Ser Asn Gly Ser Gly Ile
 225 230 235 240

30 Asn Ser Lys Glu Phe Gly Tyr Asp Lys Tyr Met Lys Gln Asn Pro Lys
 245 250 255

Ser Gln Leu Tyr Lys Met Asp Ile Arg Pro Asp Glu Phe Asn Ser Phe
 260 265 270

35 Glu Leu Ser Ala Arg Thr Tyr Glu Asn Lys Phe Thr Arg Arg Asp Ile
 275 280 285

40 Thr Ser Asp Asp Tyr Tyr Ile Lys Tyr His Tyr Thr Pro Phe Ser Glu
 290 295 300

45 Leu Ile Asp Phe Asn Val Thr Ala Ser Thr Ser Arg Gly Asn Gln Lys
 305 310 315 320

Tyr Arg Asp Gly Ser Leu Tyr Thr Phe Tyr Lys Thr Ser Ala Gln Asn
 325 330 335

50 Arg Ser Asp Ala Leu Asp Ile Asn Asn Thr Ser Arg Phe Thr Val Ala
 340 345 350

55

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Asp Asn Asp Leu Glu Phe Met Leu Gly Ser Lys Leu Met Arg Thr Arg
355 360 365

5 Tyr Asp Arg Thr Ile His Ser Ala Ala Gly Asp Pro Lys Ala Asn Gln
370 375 380

10 Glu Ser Ile Glu Asn Asn Pro Phe Ala Pro Ser Gly Gln Gln Asp Ile
385 390 395 400

Ser Ala Leu Tyr Thr Gly Leu Lys Val Thr Arg Gly Ile Trp Glu Ala
15 405 410 415

Asp Phe Asn Leu Asn Tyr Thr Arg Asn Arg Ile Thr Gly Tyr Lys Pro
420 425 430

20 Ala Cys Asp Ser Arg Val Ile Cys Val Pro Gln Gly Ser Tyr Asp Ile
435 440 445

25 Asp Asp Lys Glu Gly Phe Asn Pro Ser Val Gln Leu Ser Ala Gln
450 455 460

Val Thr Pro Trp Leu Gln Pro Phe Ile Gly Tyr Ser Lys Ser Met Arg
30 465 470 475 480

Ala Pro Asn Ile Gln Glu Met Phe Phe Ser Asn Ser Gly Gly Ala Ser
485 490 495

35 Met Asn Pro Phe Leu Lys Pro Glu Arg Ala Glu Thr Trp Gln Ala Gly
500 505 510

40 Phe Asn Ile Asp Thr Arg Asp Leu Leu Val Glu Gln Asp Ala Leu Arg
515 520 525

Phe Lys Ala Leu Ala Tyr Arg Ser Arg Ile Gln Asn Tyr Ile Tyr Ser
45 530 535 540

Glu Ser Tyr Leu Val Cys Ser Gly Gly Arg Lys Cys Ser Leu Pro Glu
545 550 555 560

50 Val Ile Gly Asn Gly Trp Glu Gly Ile Ser Asp Glu Tyr Ser Asp Asn
565 570 575

55

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Met Tyr Ile Tyr Val Asn Ser Ala Ser Asp Val Ile Ala Lys Gly Phe
 589 585 590

5 Glu Leu Glu Met Asp Tyr Asp Ala Gly Phe Ala Phe Gly Arg Leu Ser
595 600 605

Phe Gly Ala Gly Asp Ile Thr Glu Leu Pro Arg Lys Tyr Met Thr Leu
 625 630 635 640

15 Asp Thr Gly Val Arg Phe Phe Asp Asn Ala Leu Thr Leu Gly Thr Ile
645 650 655

20 Ile Lys Tyr Thr Gly Lys Ala Arg Arg Leu Ser Pro Asp Phe Glu Gln
 662 665 670

Asp Glu His Thr Gly Ala Ile Ile Lys Gln Asp Leu Pro Gln Ile Pro
 675 680 685

Thr Ile Ile Asp Leu Tyr Gly Thr Tyr Glu Tyr Asn Arg Asn Leu Thr
690 695 700

30 Leu Lys Leu Ser Val Gln Asn Leu Met Asn Arg Asp Tyr Ser Glu Ala
705 710 715 720

35 Leu Asn Lys Leu Asn Met Met Pro Gly Leu Gly Asp Glu Thr His Pro
725 730 735

Ala Asn Ser Ala Arg Gly Arg Thr Trp Ile Phe Gly Gly Asp Ile Arg
740 745 750

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Phe

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<210> 52

<211> : 133

<212> PRT

<212> ~~III~~
<213> Escherichia coli

52

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Met Ser Ser Lys Thr Lys Cys Trp Leu Trp Met Leu Leu Val Ile Leu
1 5 10 15

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Ser Glu Thr Ser Ala Thr Ser Thr Leu Lys Met Phe Asp Asn Ser Glu
 20 25 30

5
 Gly Met Thr Lys Thr Leu Leu Leu Ala Leu Ile Val Val Val Leu Tyr Cys
 35 40 45

10 Ile Cys Tyr Tyr Ser Leu Ser Arg Ala Val Lys Asp Ile Pro Val Gly
 50 55 60

15 Leu Ala Tyr Ala Thr Trp Ser Gly Thr Gly Ile Leu Met Val Ser Thr
 65 70 75 80

20 Leu Gly Ile Leu Phe Tyr Gly Gln His Pro Asp Thr Ala Ala Ile Ile
 85 90 95

25 Gly Met Val Ile Ile Ala Ser Gly Ile Ile Ile Met Asn Leu Phe Ser
 100 105 110

30 Lys Met Gly Ser Glu Glu Ala Glu Glu Thr Pro Val Thr Asn Leu Asp
 115 120 125

35 Lys Lys Ile Ala Asn
 130

<210> 53
 <211> 286
 <212> PRT
 <213> Escherichia coli
 <400> 53

40 Met Tyr Ile Lys Lys His Trp Ile Ala Leu Ser Ile Leu Leu Ile Pro
 1 5 10 15

Cys Ile Gly Asn Ala Gln Glu Ile Lys Ile Asp Glu Ser Trp Leu His
 20 25 30

45 Gln Ser Leu Asn Val Ile Gly Arg Thr Asp Ser Arg Phe Gly Pro Arg
 35 40 45

50 Leu Thr Asn Asp Leu Tyr Pro Glu Tyr Thr Val Ala Gly Arg Lys Asp
 50 55 60

Trp Phe Asp Phe Tyr Gly Tyr Val Asp Leu Pro Lys Phe Phe Gly Val
 65 70 75 80

55

5

Gly Ser His Tyr Asp Val Gly Ile Trp Asp Glu Gly Ser Pro Leu Phe
 85 90 95

Thr Glu Ile Glu Pro Arg Phe Ser Ile Asp Lys Leu Thr Gly Leu Asn
 100 105 110

10

Leu Ala Phe Gly Pro Phe Lys Glu Trp Phe Ile Ala Asn Asn Tyr Val
 115 120 125

15

Tyr Asp Met Gly Asp Asn Gln Ser Ser Arg Gln Ser Thr Trp Tyr Met
 130 135 140

20

Gly Leu Gly Thr Asp Ile Asp Thr Gly Leu Pro Ile Lys Leu Ser Ala
 145 150 155 160

25

Asn Ile Tyr Ala Lys Tyr Gln Trp Gln Asn Tyr Gly Ala Ala Asn Glu
 165 170 175

30

Asn Glu Trp Asp Gly Tyr Arg Phe Lys Ile Lys Tyr Ser Ile Pro Leu
 180 185 190

35

Thr Asn Leu Phe Gly Arg Leu Val Tyr Asn Ser Phe Thr Asn Phe
 195 200 205

Asp Phe Gly Ser Asp Leu Ala Asp Lys Ser His Asn Asn Lys Arg Thr
 210 215 220

40

Ser Asn Ala Ile Ala Ser Ser His Ile Leu Ser Leu Leu Tyr Glu His
 225 230 235 240

45

Trp Lys Phe Ala Phe Thr Leu Arg Tyr Phe His Asn Gly Gly Gln Trp
 245 250 255

50

Asn Ala Gly Glu Lys Val Asn Phe Gly Asp Gly Pro Phe Glu Leu Lys
 260 265 270

Asn Thr Gly Trp Gly Thr Tyr Thr Thr Ile Gly Tyr Gln Phe
 275 280 285

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<210> 54
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<213> Escherichia coli
<400> 54

5 Met Arg Ile Ala Pro Arg Thr Phe Phe Ala Ile Ser Ala Leu Ala Phe
1 5 10 15

Ile Val Ala Ser Gly Phe Ser Phe Trp Arg Leu Ser Pro Ala Glu Asn
10 20 25 30

Thr Gly Ile Met Ser Cys Ser Thr Lys Gly Ile Met Arg Phe Glu Asn
35 40 45

15 Met Glu Lys Glu Asn Val Asn Gly Asn Ile His Phe Asn Phe Gly Ser
50 55 60

20 Gln Gly Lys Gly Ser Met Val Leu Glu Gly Tyr Thr Asp Ser Ala Ala
65 70 75 80

Gly Trp Leu Tyr Leu Gln Arg Tyr Val Lys Phe Thr Tyr Thr Ser Lys
25 85 90 95

Arg Val Ser Ala Thr Glu Arg His Tyr Arg Ile Ser Gln Trp Glu Ser
100 105 110

30 Ser Ala Ser Ser Ile Asp Glu Ser Pro Asp Val Ile Phe Asp Tyr Phe
115 120 125

35 Met Arg Glu Met Ser Asp Ser His Asp Gly Leu Phe Leu Asn Ala Gln
130 135 140

40 Lys Leu Asn Asp Lys Ala Ile Leu Leu Ser Ser Ile Asn Ser Pro Leu
145 150 155 160

Trp Ile Cys Thr Leu Lys Ser Gly Ser Lys Leu Asp
165 170

45 <210> 55
<211> 182
<212> PRT
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50 Met Lys Ile Lys Val Ile Ala Leu Ala Thr Phe Val Ser Ala Val Phe
1 5 10 15

55

Ala Gly Ser Ala Met Ala Tyr Asp Gly Thr Ile Thr Phe Thr Gly Lys
 20 25 30

5 Val Val Ala Gln Thr Cys Thr Val Asn Thr Ser Asp Lys Asp Leu Ala
 35 40 45

10 Val Thr Leu Pro Thr Val Ala Thr Ser Ser Leu Lys Asp Asn Ala Ala
 50 55 60

15 Thr Ser Gly Leu Thr Pro Phe Ala Ile Arg Leu Thr Gly Cys Ala Thr
 65 70 75 80

Gly Met Asn Ser Ala Gln Asn Val Lys Ala Tyr Phe Glu Pro Ser Ser
 85 90 95

20 Asn Ile Asp Leu Ala Thr His Asn Leu Lys Asn Thr Ala Thr Pro Thr
 100 105 110

25 Lys Ala Asp Asn Val Gln Ile Gln Leu Leu Asn Ser Asn Gly Thr Ser
 115 120 125

30 Thr Ile Leu Leu Gly Glu Ala Asp Asn Gly Gln Asp Val Gln Ser Glu
 130 135 140

35 Tyr Ile Gly Ser Asp Gly Ser Ala Thr Leu Arg Tyr Met Ala Gln Tyr
 145 150 155 160

Tyr Ala Thr Gly Gln Ser Thr Ala Gly Asp Val Lys Ala Thr Val His
 165 170 175

40 Tyr Thr Ile Ala Tyr Glu
 180

45 <210> 56
 <211> 359
 <212> PRT
 <213> Escherichia coli
 <400> 56

50 Met Lys Arg Ile Phe Phe Ile Pro Leu Phe Leu Ile Leu Leu Pro Lys
 1 5 10 15

Leu Ala Val Ala Gly Pro Asp Asp Tyr Val Pro Ser Gln Ile Ala Val
 20 25 30

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Asn Thr Ser Thr Leu Pro Gly Val Val Ile Gly Pro Ala Asp Ala His
35 40 45

5
Thr Tyr Pro Arg Val Ile Gly Glu Leu Ala Gly Thr Ser Asn Gln Tyr
50 55 60

10 Val Phe Asn Gly Gly Ala Ile Ala Leu Met Arg Gly Lys Phe Thr Pro
65 70 75 80

15 Ala Leu Pro Lys Ile Gly Ser Ile Thr Val Tyr Phe Pro Ser Arg Lys
85 90 95

Gln Arg Asp Ser Ser Asp Phe Asp Ile Tyr Asp Ile Gly Val Ser Gly
100 105 110

20 Leu Gly Ile Ile Ile Gly Met Ala Gly Tyr Trp Pro Ala Thr Pro Leu
115 120 125

25 Val Pro Ile Asn Ser Ser Gly Ile Tyr Ile Asp Pro Val Gly Ala Asn
130 135 140

30 Thr Asn Pro Asn Thr Tyr Asn Gly Ala Thr Ala Ser Phe Gly Ala Arg
145 150 155 160

Leu Phe Val Ala Phe Val Ala Thr Gly Arg Leu Pro Asn Gly Tyr Ile
165 170 175

35 Thr Ile Pro Thr Arg Gln Leu Gly Thr Ile Leu Leu Glu Ala Lys Arg
180 185 190

40 Thr Ser Leu Asn Asn Lys Gly Leu Thr Ala Pro Val Met Leu Asn Gly
195 200 205

45 Gly Arg Ile Gln Val Gln Ser Gln Thr Cys Thr Met Gly Gln Lys Asn
210 215 220

Tyr Val Val Pro Leu Asn Thr Val Tyr Gln Ser Gln Phe Thr Ser Leu
225 230 235 240

50 Tyr Lys Glu Ile Gln Gly Gly Lys Ile Asp Ile His Leu Gln Cys Pro
245 250 255

55

140

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Asp Gly Ile Asp Val Tyr Ala Thr Leu Thr Asp Ala Ser Gln Pro Val
 260 265 270

5 Asn Arg Thr Asp Ile Leu Thr Leu Ser Ser Glu Ser Thr Ala Lys Gly
 275 280 285

10 Phe Gly Ile Arg Leu Tyr Lys Asp Ser Asp Val Thr Ala Ile Ser Tyr
 290 295 300

Gly Glu Asp Ser Pro Val Lys Gly Asn Gly Ser Gln Trp His Phe Ser
 305 310 315 320

15 Asp Tyr Arg Gly Glu Val Asn Pro His Ile Asn Leu Arg Ala Asn Tyr
 325 330 335

20 Ile Lys Ile Ala Asp Ala Thr Thr Pro Gly Ser Val Lys Ala Ile Ala
 340 345 350

25 Thr Ile Thr Phe Ser Tyr Gln
 355

30 <210> 57
 <211> 844
 <212> PRT
 <213> Escherichia coli
 <400> 57

35 Met Asn Ala Asn Asn Leu Ser Cys Leu Ile Tyr Cys Arg Cys Ser Leu
 1 5 10 15

Leu Leu Phe Ala Ala Leu Gly Leu Thr Val Thr Asn His Ser Phe Ala
 20 25 30

40 Ala Glu Glu Ala Glu Phe Asp Ser Glu Phe Leu His Leu Asp Lys Gly
 35 40 45

45 Ile Asn Ala Ile Asp Ile Arg Arg Phe Ser His Gly Asn Pro Val Pro
 50 55 60

50 Glu Gly Arg Tyr Tyr Ser Asp Ile Tyr Val Asn Asn Val Trp Lys Gly
 65 70 75 80

55 Lys Ala Asp Leu Gln Tyr Leu Arg Thr Ala Asn Thr Gly Ala Pro Thr
 85 90 95

55

Leu Cys Leu Thr Pro Glu Leu Leu Ser Leu Ile Asp Leu Val Lys Asp
 100 105 110
 5 Thr Met Ser Gly Asn Thr Ser Cys Phe Pro Ala Ser Thr Gly Leu Ser
 115 120 125
 10 Ser Ala Arg Ile Asn Phe Asp Leu Ser Thr Leu Arg Leu Asn Ile Glu
 130 135 140
 15 Ile Pro Gln Ala Leu Leu Asn Thr Arg Pro Arg Gly Tyr Ile Ser Pro
 145 150 155 160
 Ala Gln Trp Gln Ser Gly Val Pro Ala Ala Phe Ile Asn Tyr Asp Ala
 165 170 175
 20 Asn Tyr Tyr Gln Tyr Ser Ser Ser Gly Thr Ser Asn Glu Gln Thr Tyr
 180 185 190
 25 Leu Gly Leu Lys Ala Gly Phe Asn Leu Trp Gly Trp Ala Leu Arg His
 195 200 205
 30 Arg Gly Ser Glu Ser Trp Asn Asn Ser Tyr Pro Ala Gly Tyr Gln Asn
 210 215 220
 Ile Glu Thr Ser Ile Met His Asp Leu Ala Pro Leu Arg Ala Gln Phe
 225 230 235 240
 35 Thr Leu Gly Asp Phe Tyr Thr Asn Gly Glu Leu Met Asp Ser Leu Ser
 245 250 255
 40 Leu Arg Gly Val Arg Leu Ala Ser Asp Glu Arg Met Leu Pro Gly Ser
 260 265 270
 45 Leu Arg Gly Tyr Ala Pro Ala Val Arg Gly Ile Ala Asn Ser Asn Ala
 275 280 285
 Lys Val Thr Ile Tyr Gln Asn Ala His Ile Leu Tyr Glu Thr Thr Val
 290 295 300
 50 Pro Ala Gly Pro Phe Val Ile Asn Asp Leu Tyr Pro Ser Gly Tyr Ala
 305 310 315 320

55

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Gly Asp Leu Leu Val Lys Ile Thr Glu Ser Asn Gly Gln Thr Arg Met
 325 330 335

5 Phe Thr Val Pro Phe Ala Ala Val Ala Gln Leu Ile Arg Pro Gly Phe
..... 340 345 350

10 Ser Arg Trp Gln Met Ser Val Gly Lys Tyr Arg Tyr Ala Asn Lys Thr
355 . 360 . 365

Tyr Asn Asp Leu Ile Ala Gln Gly Thr Tyr Gln Tyr Gly Leu Thr Asn
 370 375 . 380

15 Asp Ile Thr Leu Asn Ser Gly Leu Thr Thr Ala Ser Gly Tyr Thr Ala
385 390 395 400

20 Gly Leu Ala Gly Leu Ala Phe Asn Thr Pro Leu Gly Ala Ile Ala Ser
405 410 415

Asp Ile Thr Leu Ser Arg Thr Ala Phe Arg Tyr Ser Gly Val Thr Arg
420 425 430

25 428 435 440 445
Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser

Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser
 435 440 445

30 Asn Thr Asn Ile Thr Leu Ala Ala Tyr Arg Tyr Ser Ser Lys Asp Phe
450 455 460

35 Tyr His Leu Lys Asp Ala Leu Ser Ala Asn His Asn Ala Phe Ile Asp
465 470 475 480

Asp Val Ser Val Lys Ser Thr Ala Phe Tyr Arg Pro Arg Asn Gln Phe
12 485 490 495

Gln Ile Ser Ile Asn Gln Glu Leu Gly Glu Lys Trp Gly Gly Met Tyr
..... 500 505 510 .. .

45 Leu Thr Gly Thr Thr Tyr Asn Tyr Trp Gly His Lys Gly Ser Arg Asn
515 520 525

50 Glu Tyr Gln Ile Gly Tyr Ser Asn Phe Trp Lys Gln Leu Gly Tyr Gln
530 535 540

Ile Gly Leu Ser Gln Ser Arg Asp Asn Glu Gln Gln Arg Arg Asp Asp

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5	Arg Phe Tyr Ile Asn Phe Thr Leu Pro Leu Gly Gly Ser Val Gln Ser 565	550	555	560
10	Pro Val Phe Ser Thr Val Leu Asn Tyr Ser Lys Glu Glu Lys Asn Ser 580	570	575	575
15	Ile Gln Thr Ser Ile Ser Gly Thr Gly Gly Glu Asp Asn Gln Phe Ser 595	600	605	
20	Tyr Gly Ile Ser Gly Asn Ser Gln Glu Asn Gly Pro Ser Gly Tyr Ala 610	615	620	
25	Met Asn Gly Gly Tyr Arg Ser Pro Tyr Val Asn Ile Thr Thr Thr Val 625	630	635	640
30	Gly His Asp Thr Gln Asn Asn Asn Gln Arg Ser Phe Gly Ala Ser Gly 645	650	655	
35	Ala Val Val Ala His Pro Tyr Gly Val Thr Leu Ser Asn Asp Leu Ser 660	665	670	
40	Asp Thr Phe Ala Ile Ile His Ala Glu Gly Ala Gln Gly Ala Val Ile 675	680	685	
45	Asn Asn Ala Ser Gly Ser Arg Leu Asp Phe Trp Gly Asn Gly Val Val 690	695	700	
50	Pro Tyr Val Thr Pro Tyr Glu Lys Asn Gln Ile Ser Ile Asp Pro Ser 705	710	715	720
55	Asn Leu Asp Leu Asn Val Glu Leu Ser Ala Thr Glu Gln Glu Ile Ile 725	730	735	
60	Pro Arg Ala Asn Ser Ala Thr Leu Val Lys Phe Asp Thr Lys Thr Gly 740	745	750	
65	Arg Ser Leu Leu Phe Asp Ile Arg Met Ser Thr Gly Asn Pro Pro Pro 755	760	765	
70	Met Ala Ser Glu Val Leu Asp Glu His Gly Gln Leu Ala Gly Tyr Val 770	775	780	

5

Ala Gln Ala Gly Lys Val Phe Thr Arg Gly Leu Pro Glu Lys Gly His
 785 790 795 800

Leu Ser Val Val Trp Gly Pro Asp Asn Lys Asp Arg Cys Ser Phe Val
 805 810 815

10

Tyr His Val Ala His Asn Lys Asp Asp Met Gln Ser Gln Leu Val Pro
 820 825 830

15

Val Leu Cys Ile Gln His Pro Asn Gln Glu Lys Thr
 835 840

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<210> 58
 <211> 277
 <212> PRT
 <213> Escherichia coli
 <400> 58

25

Met Val Lys Cys His Thr Leu Ile Asn Arg Arg Asn Lys Cys Leu Leu
 1 5 10 15

30

Ile Val Phe Ile Val Leu Ile Gly Trp Ile Ile Phe Arg Pro Lys Ala
 20 25 30

35

Tyr Thr Tyr Ser Leu Asn Asp Lys Glu Lys Glu Met Leu Ile Met Leu
 35 40 45

40

Ser Gln His Pro Glu Thr Arg Tyr Phe Gly Phe Tyr Ser Ile Glu Leu
 50 55 60

45

Pro Ala Asp Tyr Lys Pro Thr Gly Met Val Met Phe Ile Gln Gly Ser
 65 70 75 80

Ala Met Ile Pro Val Glu Thr Lys Leu Gln Tyr Tyr Pro Pro Phe Leu
 85 90 95

50

Gln Tyr Met Thr Arg Tyr Glu Ala Glu Leu Lys Asn Thr Ser Ala Leu
 100 105 110

55

Asp Pro Leu Asp Thr Pro Tyr Leu Lys Gln Val His Pro Leu Ser Pro
 115 120 125

Pro Met Asn Gly Val Ile Phe Glu Arg Met Lys Ala Lys Tyr Thr Pro

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130 135 140

5 Asp Phe Ala Arg Val Leu Asp Ala Trp Lys Trp Glu Asn Gly Val Thr
145 150 155 160

10 Phe Ser Val Lys Ile Glu Ala Lys Asp Gly Arg Ala Thr Arg Tyr Asp
165 170 175

15 Gly Ile Ser Lys Ile Ala Glu Tyr Ser Tyr Gly Tyr Asn Ile Pro Glu
180 185 190

20 Lys Lys Val Gln Leu Leu Thr Ile Leu Ser Gly Leu Gln Pro Arg Ala
195 200 205

25 Asp Asn Gln Pro Pro Ser Glu Asn Lys Leu Ala Ile Gln Tyr Ala Gln
210 215 220

30 Val Asp Ala Ser Leu Leu Gly Glu Tyr Glu Leu Ser Val Asp Tyr Lys
225 230 235 240

35 Asn Ser Asn Asn Ile Lys Ile Ser Leu Gln Thr Asp Asn Asn Ser Tyr
245 250 255

40 Ile Asp Ser Leu Leu Asp Ile Arg Tyr Pro Ser Asn Gly Asn Arg Ala
260 265 270

45 Trp Tyr Asn Ser Ile
275

40 <210> 59
<211> 366
<212> PRT
<213> Escherichia coli
<400> 59

45 Met Leu Pro Glu Pro Val Tyr Arg Arg Trp Ile Ile Leu Leu Ile Ser
1 5 10 15

50 Met Leu Thr Val Gly Thr Leu Phe Ile Leu Ser Val Trp Asn Ser Ala
20 25 30

55 Thr Tyr Trp Asp Ile Phe Ile Tyr Gly Val Leu Pro Met Leu Phe Leu
35 40 45

Trp Leu Cys Leu Phe Gly Ile Ala Leu Asn Lys Tyr Glu Gln Ser Val
 50 55 60

5 Ala Ala Cys Ile Ser Trp Glu Ser Glu Arg Gln Gln Val Lys Gln Leu
 65 70 75 80

10 Trp Gln His Trp Ser Gln Lys Gln Leu Ala Ile Val Gly Asn Val Leu
 15 85 90 95

Phe Thr Pro Glu Glu Lys Gly Met Ser Val Leu Leu Gly Pro Gln Glu
 100 105 110

15 Glu Ile Pro Ala Tyr Pro Lys Lys Ala Arg Pro Leu Phe Ser Ala Ser
 115 120 125

20 Arg Tyr Ser Leu Ser Ser Ile Phe His Asp Ile His Gln Gln Leu Thr
 130 135 140

25 Gln Gln Phe Pro Asp Tyr Arg His Tyr Leu His Thr Ile Tyr Val Leu
 145 150 155 160

30 Gln Pro Glu Lys Trp Arg Gly Glu Thr Val Arg Gln Ala Ile Phe His
 165 170 175

35 Ser Leu Tyr Asp Glu Arg Phe Asp Gly Leu Ile Leu Val Val Cys Leu
 195 200 205

40 Gln Asn Trp Pro Glu Asn Lys Pro Glu Asp Thr Ser Glu Leu Val Ser
 210 215 220

45 Ala Gln Leu Ile Ser Ser Ser Phe Val Arg Gln His Gln Ile Pro
 225 230 235 240

50 Val Ile Ala Gly Leu Gly Arg Val Met Pro Leu Glu Pro Glu Glu Leu
 245 250 255

55 Glu His Asn Leu Asp Val Leu Phe Glu Tyr Asn Gln Leu Asp Asn Lys
 260 265 270

Gln Leu Gln His Val Trp Val Ser Gly Leu Asp Glu Gly Thr Ile Glu

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275

280

285

5 Asn Leu Met Gln Tyr Ala Glu Gln His Gln Trp Ser Leu Pro Lys Lys
290 295 300

10 Arg Pro Leu His Met Ile Asp His Ser Phe Gly Pro Thr Gly Glu Phe
305 310 315 320

Ile Phe Pro Val Ser Leu Ala Met Leu Ser Glu Ala Ala Lys Glu Thr
325 330 335

15 Glu Gln Asn His Leu Ile Ile Tyr Gln Ser Ala Gln Tyr Ala Gln Lys
340 345 350

20 Lys Ser Leu Cys Leu Ile Thr Arg Lys Leu Tyr Leu Arg Thr
355 360 365

<210> 60
<211> 260
25 <212> PRT
<213> Escherichia coli
<400> 60

30 Met Leu Asn Arg Lys Leu Asn Ile Arg Leu Arg His Ser Leu Asn Ser
1 5 10 15

His Cys Ile Pro Ser Ile Ile Asn Asn Thr Val Arg Ser Phe Gln
20 25 30

35 Arg Ser Val Met Asn Thr Arg Ala Leu Phe Pro Leu Leu Phe Thr Val
35 40 45

40 Ala Ser Phe Ser Ala Ser Ala Gly Asn Trp Ala Val Lys Asn Gly Trp
50 55 60

45 Cys Gln Thr Met Thr Glu Asp Gly Gln Ala Leu Val Met Leu Lys Asn
65 70 75 80

Gly Thr Ile Gly Ile Thr Gly Leu Met Gln Gly Cys Pro Asn Gly Val
85 90 95

50 Gln Thr Leu Leu Gly Ser Arg Ile Ser Ile Asn Gly Asn Leu Ile Pro
100 105 110

55

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Thr Ser Gln Met Cys Asn Gln Gln Thr Gly Phe Arg Ala Val Glu Val
115 120 125

5 Glu Ile Gly Gln Ala Pro Glu Met Val Lys Lys Ala Val His Ser Ile
130 135 140

10 Ala Glu Arg Asp Val Ser Val Leu Gln Ala Phe Gly Val Arg Met Glu
145 150 155 160

Phe Thr Arg Gly Asp Met Leu Lys Val Cys Pro Lys Phe Val Thr Ser
165 170 175

15 Leu Ala Gly Phe Ser Pro Lys Gln Thr Thr Ile Asn Lys Asp Ser
180 185 190

20 Val Leu Gln Ala Ala Arg Gln Ala Tyr Ala Arg Glu Tyr Asp Glu Glu
195 200 205

25 Thr Thr Glu Thr Ala Asp Phe Gly Ser Tyr Glu Val Lys Gly Asn Lys
210 215 220

Val Glu Phe Glu Val Phe Asn Pro Glu Asp Arg Ala Tyr Asp Lys Val
225 230 235 240

30 Thr Val Thr Val Gly Ala Asp Gly Asn Ala Thr Gly Ala Ser Val Glu
245 250 255

35 Phe Ile Gly Lys
260

40 <210> 61
<211> 385
<212> PRT
<213> Escherichia coli
<400> 61

45 Val Val Ile Ile Asn Ser Thr Ile Leu Ser Gly Ala Gly Ala Ile Pro
1 5 10 15

50 Ser Leu Thr Ser Leu Leu Pro Asp Ile Arg Lys Met Leu Leu Val Thr
20 25 30

Asp Arg Asn Ile Ala Gln Leu Asp Gly Val Gln Gln Ile Arg Ala Leu
35 40 45

55

Leu Glu Lys His Cys Pro Gln Val Asn Val Ile Asp Asn Val Pro Ala
 50 55 60

5

Glu Pro Thr His His Asp Val Arg Gln Leu Met Asp Ala Pro Gly Asp
 65 70 75 80

10

Ala Ser Phe Asp Val Val Val Gly Ile Gly Gly Ser Val Leu Asp
 85 90 95

15

Val Ala Lys Leu Leu Ser Val Leu Cys His Pro Gln Ser Pro Gly Leu
 100 105 110

20

Asp Ala Leu Leu Ala Gly Glu Lys Pro Thr Gln Arg Val Gln Ser Trp
 115 120 125

25

Leu Ile Pro Thr Thr Ala Gly Thr Gly Ser Glu Ala Thr Pro Asn Ala
 130 135 140

30

Ile Leu Ala Ile Pro Glu Gln Ser Thr Lys Val Gly Ile Ile Ser Gln
 145 150 155 160

35

Val Leu Leu Pro Asp Tyr Val Ala Leu Phe Pro Glu Leu Thr Thr Ser
 165 170 175

40

Met Pro Ala His Ile Ala Ala Ser Thr Gly Ile Asp Ala Leu Cys His
 180 185 190

45

Leu Leu Glu Cys Phe Thr Ala Thr Val Ala Asn Pro Val Ser Asp Asn
 195 200 205

50

Ala Ala Leu Thr Gly Leu Ser Lys Leu Phe Arg His Ile Gln Pro Ala
 210 215 220

55

Val Asn Asp Pro Gln Asp Leu Arg Ala Lys Leu Glu Met Leu Trp Ala
 225 230 235 240

Ser Tyr Tyr Gly Gly Val Ala Ile Thr His Ala Gly Thr His Leu Val
 245 250 255

55

His Ala Leu Ser Tyr Pro Leu Gly Gly Lys Tyr His Leu Pro His Gly
 260 265 270

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Val Ala Asn Ala Ile Leu Leu Ala Pro Cys Met Ala Phe Val Arg Pro
275 280 285

5 Trp Ala Val Glu Lys Phe Ala Arg Val Trp Asp Cys Ile Pro Asp Ala
290 295 300

10 Glu Thr Ala Leu Ser Ala Glu Glu Lys Ser His Ala Leu Val Thr Trp
305 310 315 320

Leu Gln Ala Leu Val Asn Gln Leu Lys Leu Pro Asn Asn Leu Ala Ala
325 330 335

15 Leu Gly Val Pro Pro Glu Asp Ile Ala Ser Leu Ser Glu Ala Ala Leu
340 345 350

20 Asn Val Lys Arg Leu Met Asn Asn Val Pro Cys Gln Ile Asp Leu Gln
355 360 365

25 Asp Val Gln Ala Ile Tyr Gln Thr Leu Phe Pro Gln His Pro Phe Lys
370 375 380

Glu
385

30 <210> 62
<211> 105
<212> PRT
<213> Escherichia coli
35 <400> 62

Met Asn Ile Arg Lys Leu Phe Cys Pro Gly Asn Thr Pro Arg Ile Leu
1 5 10 15

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Claims

1. Isolated antigenic polypeptides selected in the group comprising SEQ ID N°11 to SEQ ID N°66 and the homologous sequences.
- 5 2. Isolated antigenic polypeptides according to claim 1 obtainable by a process comprising the steps of:
 - 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria,
 - 10 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
 - 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates,
 - 4- testing the polypeptides for immunogenicity using animals models.
- 15 3. Isolated polynucleotides, coding for a polypeptide according to claim 1 or 2, according to the universal genetic code.
4. Isolated polynucleotides according to claim 3, having sequences selected in the group comprising SEQ ID N°77 to SEQ ID N°132.
- 20 5. An expression vector comprising at least an isolated polynucleotide according to claim 3 or 4.
6. A host cell comprising an expression vector according to claim 5.
- 25 7. A process for isolating and identifying antigenic polypeptides, useful as vaccines comprising the steps of:
 - 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria,
 - 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
 - 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates,
 - 4- testing the polypeptides for immunogenicity using animals models.
- 30 8. The process of claim 7, comprising the use of infected adult animals, eventually immunodepressed, and of infant animals as models for neonatal infections.
9. The use of at least one polypeptide selected in the group comprising SEQ ID N°1 to SEQ ID N°66 as antigens and the homologous sequences.
- 35 10. A vaccine composition specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide such as selected by the process of claim 7, alone or in combination, particularly at least one polypeptide having a sequence selected in the group comprising SEQ ID N°1 to SEQ ID N°66 and the homologous sequences, with a carrier.
11. The vaccine composition of claim 10 for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.
- 40 12. The vaccine composition of claim 10 or 11, adapted to specific indication in combination with components directed against other bacteria, such as *S.aureus* or group B *Streptococcus*.
13. Antibodies or fragments thereof directed against a polypeptide such as used according to claim 9.
- 45 14. A method for detecting the present or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection, comprising the use of at least one polypeptide such as defined in claim 9, or a polynucleotide according to claim 3 or 4, or an antibody to claim 13.
15. Pharmaceutical composition for alleviating and/or preventing and/or treating and undesirable growth of *E. coli* comprising an effectiveness of at least one polypeptide such as use in claim 9.



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 02 29 0556
shall be considered, for the purposes of subsequent
proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant - to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	WO 01 66572 A (INST NAT SANTE RECH MED ;NASSIF XAVIER (FR); TINSLEY COLIN (FR); B) 13 September 2001 (2001-09-13) SEQ ID NOS:347 and 348 * page 3, line 20 - page 4, line 17 * * page 29, line 23 - line 31 * ---	1-6,9-15	C12N15/31 C12N15/63 C07K14/245 C07K16/12 A61K39/108 G01N33/53
A	JOHNSON JAMES R ET AL: "Phylogenetic and pathotypic similarities between Escherichia coli isolates from urinary tract infections in dogs and extraintestinal infections in humans." JOURNAL OF INFECTIOUS DISEASES, vol. 183, no. 6, 2001, pages 897-906, XP002211433 ISSN: 0022-1899 * abstract * ---	-/-	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
			C12N C07K
INCOMPLETE SEARCH			
The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.			
Claims searched completely :			
Claims searched incompletely :			
Claims not searched :			
Reason for the limitation of the search:			
see sheet C			
Place of search	Date of completion of the search	Examiner	
THE HAGUE	28 August 2002	Mata-Vicente, M	
CATEGORY OF CITED DOCUMENTS		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons R : member of the same patent family, corresponding document	
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document			



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SHEET C

Application Number
EP 02 29 0556

As far as an "in vivo" method is concerned claim 9 is directed to a method of treatment of the human/animal body (Article 52(4) EPC) and the search has been carried out and based on the alleged effects of the compound/composition.

As far as an "in vivo" method is concerned claim 14 is directed to a diagnostic method practised on the human/animal body (Article 52(4) EPC) and the search has been carried out and based on the alleged effects of the compound/composition.



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 02 29 0556

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	TECHNICAL FIELDS SEARCHED (Int.Cl.7)
A	<p>MUEHLDORFER I ET AL: "Characterization of Escherichia coli strains isolated from environmental water habitats and from stool samples of healthy volunteers." RESEARCH IN MICROBIOLOGY, vol. 147, no. 8, 1996, pages 625-635.</p> <p>XP002211434</p> <p>ISSN: 0923-2508</p> <p>* table 1 *</p> <p>* page 630, paragraph 2 *</p> <p>-----</p>		



European Patent
Office

Application Number

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:



European Patent
Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 02 29 0556

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: Claims (1-6 and 9-15) - partially

Isolated antigenic polypeptide SEQ ID NO:11; the polynucleotide encoding it (SEQ ID NO:77); vector comprising said polynucleotide and host cell transformed with it; antibodies against said polypeptide; vaccines comprising the polypeptide; methods of diagnosis/treatment derived of the use of any of the molecules previously mentioned.

Inventions 2-56: Claims (1-6 and 9-15) - partially

Idem as invention 1, but restricted to each one of the polypeptides of SEQ ID NOS:12-66 and their corresponding genes (SEQ ID NOS:78-132).

Invention 57: Claims (9-15) - partially

Use of the polypeptide SEQ ID NO:1 as antigen; vaccines; antibodies against said polypeptide; methods of diagnosis/treatment derived of the use thereof.

Inventions 58-66: Claims (9-15) - partially

Idem as invention 57, but restricted to each one of the polypeptides SEQ ID NOS:2-10.

Invention 67: Claims (7 and 8) - partially

Process for isolating and identifying polypeptides useful as vaccines comprising the steps of: selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria; identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates; purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates; and testing the polypeptides for immunogenicity using animal models.

ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.

EP 02 29 0556

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

28-08-2002

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
WO 0166572	A	13-09-2001	FR WO	2806096 A1 0166572 A2
				14-09-2001 13-09-2001

EPO FORM P0458

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2005/002105

A. CLASSIFICATION OF SUBJECT MATTER					
IPC 7	A61K39/108	A61K39/10	A61K39/112	A61K39/106	A61K39/39
	A61K39/02	A61K39/00			

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, Sequence Search, BIOSIS, WPI Data, PAJ, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EP 1 342 784 A (MUTABILIS S.A) 10 September 2003 (2003-09-10) paragraph '0031! - paragraph '0034! claim 10 sequence 9	1-10
A	DATABASE UniProt 'Online! 1 November 1996 (1996-11-01), "Cytotoxic necrotizing factor 1." XP002323706 retrieved from EBI accession no. UNIPROT:Q47106 Database accession no. Q47106 the whole document	1-10

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 June 2005	26.08.2005
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel: (+31-70) 340-2040, Tx: 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Ulbrecht, M

INTERNATIONAL SEARCH REPORT

International Application No PCT/EP2005/002105

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MOREAU VIOLAINE ET AL: "Actin can reorganize into podosomes in aortic endothelial cells, a process controlled by Cdc42 and RhoA." MOLECULAR AND CELLULAR BIOLOGY, vol. 23, no. 19, October 2003 (2003-10), pages 6809-6822, XP002323705 ISSN: 0270-7306 abstract page 6810, left-hand column, paragraph 6	1-10
T	MUNRO P ET AL: "The Rho GTPase activators CNF1 and DNT bacterial toxins have mucosal adjuvant properties" VACCINE, BUTTERWORTH SCIENTIFIC. GUILDFORD, GB, vol. 23, no. 20, 8 April 2005 (2005-04-08), pages 2551-2556, XP004789509 ISSN: 0264-410X the whole document	1-9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2005/002105

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-10 (completely)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-10 (all completely)

A vaccine composition comprising an immunoadjuvant compound consisting of a Rho GTPase activator.

Invention 2: claims 11-13 (all partially)

A protein comprising a polypeptide consisting of the injection domain of a Rho GTPase activator comprising residues 1-719 of SEQ ID No. 1 and the catalytic domain of a Rho GTPase activator comprising residues 720-1014 of SEQ ID No. 1; the use of said polypeptide or of a polypeptide according to SEQ ID No. 1 for manufacturing a vaccine composition.

Invention 3-4: claims 11-13 (all partially)

Idem as invention 3, but each of invention 3 and 4 referring to SEQ ID Nos. 2 and 3, respectively.

Invention 5: claims 11-13 (all partially)

A protein comprising a polypeptide consisting of the injection domain of a Rho GTPase activator comprising residues 1-1145 of SEQ ID No. 4 and the catalytic domain of a Rho GTPase activator comprising residues 1145-1451 of SEQ ID No. 4; the use of said polypeptide or of a polypeptide according to SEQ ID No. 4 for manufacturing a vaccine composition.

Inventions 7-10: claim 11-13 (partially)

Idem as invention 6, but each of the inventions 7-10 referring to one of SEQ ID Nos. 6-9.